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SEARCH REQUEST FORM

Scientific and Technical Information Center

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Mail Box and Bldg/Room Location	Number 30	Serial Number:	
Mail Box and Bldg/Room Location		Results Format Preferred (circ	cle): PAPER DISK E-MA
If more than one search is subm	itted, please pric	pritize searches in order of	need.
Please provide a detailed statement of the sinclude the elected species or structures, kutility of the invention. Define any terms to known. Please attach a copy of the cover since	search topic, and desc eywords, synonyms, that may have a speci-	cribe as specifically as possible the acronyms, and registry numbers, an	subject matter to be searched.
Title of Invention:			
Inventors (please provide full names):			
	 		
Earliest Priority Filing Date:		•	
For Sequence Searches Only Please include ppropriate serial number.	e all pertinent informat	ion (parent, child, divisional, or issued	d patent numbers) along with the
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PTO-1590 (8-01)

Other

Online Time:

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BioTech-Chem Library Search Results Feedback Form (Optional)

Voluntary Results Feedback Form

Other Comments:



The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact the BioTech-Chem searcher who conducted the search or contact:

Mary Hale, Supervisor, 308-4258 CM-1 Room 1E01

>	I am an examiner in Workgroup: (Example: 1610)
>	Relevant prior art found, search results used as follows:
	102 rejection
-	103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
×	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Search results were not useful in determining patentability or understanding the invention.

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or e-mail mary.hale@uspto.gov.

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

February 8, 2003, 10:28:18; Search time 14 Seconds (without alignments)
34.334 Million cell updates/sec

US-09-251-073A-16 23

1 BILDV 5 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

o Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* **Database** :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description G Query Score Match Length DB

Result No.

No matches found

Search completed: February 8, 2003, 10:30:21 Job time : 14 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2003, 10:25:23; Search time 11 Seconds (without alignments) 18.853 Million cell updates/sec Run on:

US-09-251-073A-16 23

1 BILDV 5 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ü Query Score Match Length DB No. Result

Description

Search completed: February 8, 2003, 10:29:25 Job time : 11 secs

No matches found

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GenCore version 5.1.3
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OM protein - protein search, using sw model
                Run on:
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US-09-251-073A-16 23

1 EILDV 5 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries

SPTREMBL 21:*

Database :

sp arches:*
sp_bacteria:*
sp_fung1:*
sp_human.*
sp_invertebrate:*
sp_mammal:*
sp_organelle:*
sp_phage:*

plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* sp archeap:*

12:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Query Score Match Length DB

Description

No matches found

Search completed: February 8, 2003, 10:30:00 Job time : 28 secs

OM protein - protein search, using sw model

February 8, 2003, 10:25:08 ; Search time 33 Seconds Run on:

(without alignments) 20.189 Million cell updates/sec

US-09-251-073A-16 23

1 BILDV 5 Perfect score: Seguence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

1

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 100% Maximum Match 100%

Listing first 100 summaries

Database

.DAT:* .DAT: DAT: DAT /gcgdata/geneseq/genesegp-embl/AA1989. /gcgdata/geneseq/genesegp-embl/AA1990. | SIDS2/gcddata/geneseq/geneseqp-embl/AA1981.1 | SIDS2/gcddata/geneseq/geneseqp-embl/AA1982.1 | SIDS2/gcddata/geneseq/geneseqp-embl/AA1983.1 | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.1 | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.1 | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.1 | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.1 | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.1 | SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.1 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992 /SIDS2/gcgdata/geneseg/genesegp-embl/AA1993 /SIDS2/gcgdata/geneseg/genesegp-embl/AA1994 /gcgdata/geneseq/geneseqp-emb1/AA1980. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199 A_Geneseq_101002:* :_/SIDS2/gcgdata/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997

Fibronectin CS1-de VLA-4 inhibitor pe Fibronectin VLA-4 Fibronectin fragme Integrin recogniti LDV-peptide capabl Peptide recognised Alpha-4Beta-1 inte Integrin ligand di Cell adhesion pept Description SUMMARIES AAY80488 AAY77442 AAY69619 AAB73465 AAB91966 AAB50876 AAW46318 AAY03855 AAR95719 AAW25192 ü 222113 DB Query Match Length 100.0 100.0 100.0 100 Score Result

AAB59135 22 S 100.0 23 1

Peptide #3 recogni

ALIGNMENTS

RESULT 1 AAR95719

AAR95719 standard; peptide; 5 AA.

AAR95719;

(first entry) 04-DEC-1996

Alpha-4Beta-1 integrin binding inhibitory peptide 16.

VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4; inhibitor; binding; white blood cell; migration; capillary wall; tissue damage; injury; fibronectin; extracellular matrix glycoprotein; CS1; CS5; H1; LDV; active site.

Synthetic.

Location/Qualifiers Key Modified-Bite

/note= "Val-NH2"

US5510332-A

23-APR-1996

94US-0271830 07-JUL-1994;

94US-0271830 07-JUL-1994;

Vanderslice P; Ren K, Kogan TP, Beck PJ,

(TEXA-) TEXAS BIOTECHNOLOGY CORP.

WPI; 1996-221274/22.

New peptide(s) based on the LDV domain of fibronectin - used for inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or invasin

Disclosure; Column 21-22; 35pp; English.

Surface of endothelial cells that line the interior wall of capillaries ourface of endothelial cells that line the interior wall of capillaries. C. VCAM-1 recognises and binds to the integrin alpha-debeta-1 (IAAB1) or VCAM-1 correction to the capillary and a betteroid meric protein present on the surface of certain white blood cells to adhere to the capillary wall in areas where the tissue surrounding the capillary has been infected or damaged. Sometimes this white blood cells migration can become uncontrolled, with white blood cells flooding to the scene, causing widespread tissue damage. Cops. capable of blooding to the scene, causing widespread tissue damage. Cops. capable of blooding to the scene, causing widespread tissue damage. It is the stracellular matrix glycoprotein floronectin. Three distinct IAAB1-binding sites have been identified with fibronectin. One site is found in the Hepli region and is capable and contains the tripopide LDV as its minimal active affinity for IAAB1 and contains the tripopide LDV as its minimal active affinity for IAAB1 and contains the tripopide LDV as its minimal active site. Peptides AAR95704-805 are modeled after a portion of the CSI peptide that include the LDV domain presented in such a way by its novel flanking sequence to produce a potent inhibitor of IAAB1 binding.

5 AA; Sequence

Gaps ö Query Match 100.0%; Score 23; DB 17; Length 5; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 5; Conservative 0; Mismatches 0; Indels

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Bruder JT,
                                                                                                                                                                         WPI; 1998-119984/11.
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                             (GENV-) GENVEC INC
                                                                                                                                                                                                                                                                                                                                                                                        5 AA;
                                                                                          17-APR-1996;
                                                                                                           08-SEP-1994;
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                                                      US5712136-A
                                                                        27-JAN-1998
                                                                                                                                               Brough DE,
Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EILDV
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                  AAW25187-W25192 are peptides containing an LDV sequence or equivalent. The peptides are capable of binding to cell adhesion molecules and are used in aqueous irrigation solutions for use during and after endoscopic operations. Preferred irrigation solutions are electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing the amino acid sequences: RGD, LDV, DA, DGBA, GPRP, VTL, YIGSR, KQAGDV and/or RBDV (given in one letter amino acid code). The solutions are especially used for irrigating the bladder during and after tumour removal by transurethral resection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                    LDV; leucine; aspartic acid; valine; cell adhesion molecule;
binding; bladder irrigation; tumour removal; endoscopic operation;
transurethral resection; cancer; neoplasia.
                                                                                                                                                                                                                                                                                                                        Endoscopic irrigation solns. - contg. peptide(s) that bind to cell adhesion molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibrinogen; integrin; alpha-IIb-beta3; cell surface receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 18; Length 5; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                   LDV-peptide capable of binding cell adhesion molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptides protect against recurrence of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide recognised by integrin alpha4etal.
                                                              AAW25192 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW46318 standard; Protein; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 8; 8pp; German.
                                                                                                                                                                                                                                                 95DE-1029909,
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
Then 5; Conserve
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                                                                                                                                                                                                                                                                                                      WPI; 1997-133793/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AA;
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                                                                                                                                                                                                                               15-AUG-1995;
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                                                                                                  05-JAN-1998
                                                                                                                                                                                                             20-FEB-1997,
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           EILDV
EILDV
                                                                                                                                                                         Synthetic
                                                                                 AAW25192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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The present sequence is a linear stretch of amino acids (present in fibronectin) recognised by the integrin alpha4betal. Integrins are cell bronectin) recognised by the integrin alpha4betal. Integrins are cell brones. The integrins of the cast proteins of adenoviruses binds to integrins. The integrins not only proteins of adenoviruses binds to integrins. The integrins not only proteins of adenoviruses binds to the extracellular matrix molecules. The mediate cellular adhesion to the extracellular matrix molecules. The acell in vitro having a particular cell surface binding site. The acell in vitro having a particular cell surface binding site. The adenovirus and a second component that selectively binds a binding domain of the penton base protein of the adenovirus and a second component that selectively binds the cell surface binding site. A complex of the adenovirus and the cell surface binding site. The adenovirus into the cell is contacted with it to allow entry of the adenovirus into the cell. The methods can be used for research and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
penton base protein; coat proteins; adenovirus; binding site; cellular adhesion; extracellular matrix molecule; binding domain; cell surface binding site; bispecific molecule; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methods for introducing adenovirus into cells - used for genetic engineering and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kovesdi I, McVey DL, Roelvink PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 19; Length 5; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Column 2; 56pp; English
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                                                                                                                                                                                                                                                                                                         in existing platelet thrombus in a blood vessel is due to dissociation of fibrinogen from glycoprotein IIb-IIIa. This dissociation is caused by the binding of an integrin-ligand dissociation provides a method of disaggregating an existing platelet thrombus in a blood vessel, where the platelet comprises an existing platelet thrombus in a blood vessel, where the platelet comprises administering a compound which dissociates fibrinogen bound to a first site on platelet glycoprotein IIb-IIIa, by binding to a second interacting at compound which dissociates fibrinogen bound to a first site on platelet glycoprotein IIb-IIIa, by binding to a second interacting atte on platelet glycoprotein IIb-IIIa, by binding to a second interacting atte on platelet glycoprotein IIb-IIIa, and saggragating the platelet thrombus. The method is used to treat humans with unstable angina, stroke and/or acute myocardial infarction. The methods can be used to enact de-adhesion of osteoclasts from the bone surface to halt bone loss in a patient with osteoporcesis. The methods can also be used for the de-adhesion of angiogenic endothelial cells in a patient with a pathology. Condution associated with angiogenesis, e.g. cancer, diabetic retinopathy, psoriasis. The methods and also be used to treat tumours, atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory bowel disease, or organ transplant rejection, and aethma. The methods can be used for the dissolution of pre-formed platelet aggregates, which is a departure from the current strategy of treatment prior to formation of the processes of the processes and interaction of the plate of the plat
                                                                                                                                                                                                                                                                                                The invention relates to integrin ligand dissociators. Disaggregation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bone regenerative; osteopathic; osseous tissue; reconstitution; scaffold matrix; bone formation promoter; bone resorption inhibitor; cell adhesion; osteoblast; osteoclast; bone defect; fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dissociator (ILD) that can be used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 20; Length 5; 100.0%; Pred. No. 7.8e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                     Disaggregating a ligand:integrin receptor complex
                                                                                                                                                                                                                                                           Disclosure, Page 10; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY80488 standard; peptide; 5 AA
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                                                                                                           (BURN-) BURNHAM INST
                                                                                                                                                                                  WPI; 1999-243586/20
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ses 5; Conserv
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                                    03-SEP-1998;
                                                                         03-SEP-1997;
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 11-MAR-1999.
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                                                                                                                                              Hu DD,
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Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The system is used to replace, remodel or correct bone defects, e.g. fractures, fissures or bone mass loss. Incorporation of (1) into the scaffold results in rapid seeding by osteoblasts and the development of an organic matrix, i.e. the preformed scaffold replaces the rate-determining step of extracellular matrix formation. The scaffold car be designed to have a predetermined resorption/degradation rate, and may include regulatory compounds for specific cell types.
                                                                                                                                                                            System for reconstructing osseous tissue, useful e.g. for treating fractures, comprises scaffold containing promoter of bone formation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                 The invention relates to a novel system for reconstitution of osseous tissue comprising a scaffold carrying a compound (I) that promotes bone formation and a component that decreases bone resorption (II).

(I) induces migration and adhesion of osteoblasts and osteoclasts and (II) inhibits proteolysis (specifically by plasmin) of extracellular matrix. (I) is preferably selected from: selectin or selectin binding fragments, proteins and peptides that facilitate call adhesion, plasminogen activator inhibitors. The poptides ANY80466-Y80492 are claimed metalloprocease inhibitors. The poptides ANY80466-Y80492 are claimed examples of cell adhesion peptides used in the system of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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                                           (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibronectin CS1-derived peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY77442 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                          Claim 14; Page 32; 44pp; English
                                                                                                                                                                                                                                 inhibitor of bone resorption -
98US-0122348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US26605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
1es 5; Conservative
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                                                                                                                                    WPI; 2000-195084/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s AA;
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24-JUL-1998;
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1 BILDV
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                                                                                        Budny JA;
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                                                                                                      The invention relates to peptidomimetic compounds (AAY77415-Y77438)

capable of inhibiting the binding of the VLA-4 integrin (alpha 4-beta-1, CD494(CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the surface of leukcytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukcyte adhesion to the CS-1 FN/VLA-4 interaction plays an important role in the inflammacory response. The peptidomimetics of the critical step in the inflammacory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatory activities, osteoarthritis and other skin inflammations, demyelinating diseases of the central nervous system conditions acterosis), allergies, atheroselerosis, colitie, diabetes, inflammatory bowel disease, atheroselerosis, colitie, diabetes, inflammatory bowel disease, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to comparison to the CS-1 peptide and therefore less expensive to the CS-1 peptide the CS-1 peptide to immobilised CS-1 peptide the CAS-1 peptide to inthibit VLA-4 Unrkat cells to immobilised CS-1 peptide
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peptidomimetic compounds used as cell surface fibronectin essing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1; CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative; arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder; autolmmune disorder; respiratory disorder; LDV motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 21;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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                                                                            Disclosure, Fig 2; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY69619 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLA-4 inhibitor peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                         cardiovascular disorders
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200000477-A1.
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The invention relates to novel arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives and related compounds (1), and their salts and prodrugs. These are are integrin inhibitors, specifically of salts and prodrugs. These are are integrin inhibitors, specifically of VLA-4 (very late annigen 4, also known as alpha-4-beta-1 or CD494G/CD29), which mediate cell adhesion. VLA-4 is a receptor for the cytokine-inducible cell surface protein VCAM-1 (vascular cell adhesion molecule-1) and for the alternatively spliced forms of fibronectin (FN) which contain the CS-1 domain. The novel compounds inhibit cell adhesion, and consequent or associated pathogenic processes mediated by VLA-4, and man their caspiratory disorders. These include asthma, arthritis, sutchimmune, or respiratory disorders. These include asthma, arthritis, sutchimmatory bowel disease. Sequences AAVS6918-V69502 represent peptides derived from the VLA-4-binding domain of the FN CS-1 region which contain the LDV motif and are known to inhibit fibronectin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin antagonist, VLA-4 antagonist, alpha-4-beta-1 integrin; every late antigen; antibody; kidney disease; chronic renal failure; end-stage renal disease; chronic diabetic nephropathy; diabetic alomerulopathy; diabetic renal hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertensive nephrosclerosis, hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary nephritis, renal dysplasia, nephrotropic, cell adhesion inhibition, fibronectin CS-1 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating a mammal in, or at a risk of developing, chronic renal failure, involves administering at least one integrin antagonist
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Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 21; Length 5; Similarity 100.0%; Pred. No. 7.8e+05; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibronectin VLA-4 binding domain-derived pentapeptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNLO ) IMPERIAL COLLEGE SCI TECHNOLOGY & MED
                                   Disclosure; Page 2; 120pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB73465 standard; peptide; 5 AA.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                       5 AA;
                                                                                                                                                                                                                                                                                                                                                                 cell adhesion.
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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us-09-251-073a-16.closed.rag

The invention relates to a method for treating a mammal with, or at risk of developing, chronic renal failure, involving the administration of at least one integrin antegonist. The integrin antagonists that may be used in the method include antagonists of alpha-4-subunit containing integrins or antagonists of alpha-1-subunit containing integrins or antagonists of alpha-1-subunit containing integrins. In particular, the antagonists of alpha-1-subunit containing integrins. In particular, the antagonists of alpha-1-subunit integrin and tite organte aligand (collagen IV, and laminin in the case of VLA-1, and fibronectin and VCAV-1 in the case of VLA-4). The method of the invention may be used to treat chronic renal failure, and exage renal disease, chronic diabetic nephropathy, diabetic nephrosts, opportensive glomerulosalerosis, chronic glomerulonephritis, hereditary nephritis or renal dysplasia. Sequences AAR73466-AAR3466 represent periodes derived from the VLA-4 binding domain (CS-1 region) of therefore be used in the method of the invention. ö The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity Gaps Protection, endogenous therapeutic peptide; peptidase, conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter. ö Fibronectin fragment and fibrin related peptide SEQ ID NO:1142. Length 5; Thibaudeau Indels 100.0%; Score 23; DB 22; 100.0%; Pred. No. 7.8e+05; tive 0; Mismatches 0; Holmes DL, Disclosure; Page 569; 733pp; English. Bridon DP, Ezrin AM, Milner PG, AAB91966 standard; Peptide; 5 AA. 99US-0134406. 99US-0153406. 99US-0159783. 17-MAY-2000; 2000WO-US13576. (first entry) Conservative (CONJ-) CONJUCHEM INC. WPI; 2001-112059/12. Local Similarity 5 AA; WO200069900-A2 S Homo sapiens 17-MAY-1999; 10-SEP-1999; 22-JUN-2001 15-OCT-1999; 23-NOV-2000 1 EILDV Synthetic. AAB91966; Seguence Query Match Matches AAB91966 RESULT 셤 ઠ

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bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. It] are useful for modifying therapeutic peptidas e.g. hormonase, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes AAB90829 to AAB92441 represent peptides with physiological processes. exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin; immunosuppressive; inflammatory bowel disease; arthritis; multiple sclerosis; asthma; atherosclerosis; wound healing.
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                                                                                                                                                                                                                                                                                                                                          Length 5;
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                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 22; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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responses by contacting the structural model with paxillin or a paxillin related molecule in the presence and absence of a test agent and determining binding of paxillin or paxillin related molecule to the structural model. A decrease in binding in the presence of the test agent indicates that the test agent is an inhibitor of alpha4 integrin biological response. Inhibitors of the binding of paxillin to alpha4 are useful in blocking immune responses in conditions such as inflammatory bowel disease, arthritis, multiple sclerosis and asthma and in inhibiting atherosclerosis and scarring during wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Score 23; DB 22; Length 5; Pred, No. 7.8e+05;

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Best Local Similarity

thrombosis and malignancy.

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Sequence Query Match

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US-09-320-907B-3
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Sequence 3, Appli
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10.077 Million cell updates/sec
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| Patent No. US20020159998A1
| GENERAL INFORMATION:
| APPLICANT: MUNDY, GREGORY R.
| APPLICANT: YONEDA, TOSHIYUKI
| TITLE OF INVENTION: METHODS OF TREATING MULTIPLE MYELOWA AND
| TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN
| FILE REFERENCE: A061CIP2
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/BCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_REMECOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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9 US-09-320-907B-3
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Listing first 100 summaries
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                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Score Match Length DB ID
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APPLICANT: GINSBERG, MARK H.
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
FILE REFERENCE: STR.0006
CURRENT APPLICATION NUMBER: US/09/320,907B
CURRENT FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 09/187,236
PRIOR PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: 926 ID NOS: 25
SEQ ID NO 3
LENGTH: 5
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US-10-086-217-6
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Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 09/943,659
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/805,840
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/100,182
PRIOR PILING DATE: 1998-09-14
PRIOR PILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATCHIN VET: 2.1
SEQ ID NO 6
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 5; Conservative
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Score 23; DB 1; 1
Pred. No. 1.9e+05;
                                                                    COMPUTER READABLE FORM:
MEDUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/109,106
FILING DATE:
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/725,668
FILING DATE: July 3, 1991
ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REJESTRATION NUMBER: 33,367
RESISTRATION NUMBER: 33,367
REJESTRATION NUMBER: 33,367
REJESTRATION NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington
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FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-109-106-3
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SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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IDENTIFICATION METHOD:
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PUBLICATION INFORMATION:
AUTHORS:
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DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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MAP POSITION:
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Best Local Similarity
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POSITION IN GENOME:
                                      STATE: D.C. COUNTRY: U.S.A.
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ISSUE:
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                                                                                                                               February 8, 2003, 10:28:33 ; Search time 14 Seconds (without alignments) 10.508 Million cell updates/sec
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Sequence 3, P
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Sequence 2
Sequence 2
Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sued Patents AA:*
/cgn2 6/ptodata1/jaa/5A_COMB.pep:*
/cgn2 6/ptodata1/jaa/5B_COMB.pep:*
/cgn2 6/ptodata1/jaa/6A_COMB.pep:*
/cgn2 6/ptodata1/jaa/6B_COMB.pep:*
/cgn2 6/ptodata1/jaa/6B_COMB.pep:*
/cgn2 6/ptodata1/jaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata1/jaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                           12
                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-303-162A-3
US-08-634-060-3
US-08-38-282-10
US-08-709-515-3
US-08-709-846-2
US-09-146-203-3
US-08-983-391-2
US-08-983-372-2
US-08-376-372-2
US-08-375-321-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-07542-3
                                                                                                                                                                                                                                                                                                                                                   262574 segs, 29422922 residues
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Patent No. 5475100
GENERAL INFORMATION:
APPLICANT: Kimikazu HASHINO et al.
TITLE OF INVENTION: Artificial Antibody
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 100 summaries
                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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23
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Match Length
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100.0 100.0

Score

Result Š US-08-109-106-3

Minimum DB seq length: 0 Maximum DB seq length: 5

Issued

Database

BLOSUM62

Scoring table:

Searched:

Perfect score:

Sequence:

OM protein

Run on:

Length 5;

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STREET: Two Prudential Plaza, Suite 4900
CITY. Chicago
STATE: The Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                PILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION NUMBER: 304
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTAATION NUMBER: 30763
REPERENCE/DOCKET NUMBER: 71602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/402,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-634-060-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                          STATE: Illinois
COUNTRY: USA
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US-08-338-282-10
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                  Gaps
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Sequence 3, Application US/08634060
Patent No. 5712136
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Koveedi, Imre
APPLICANT: Roelvink, Petrus W.
TITLE OF INVENTION: THE ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY TITLE OF INVENTION: THE ADENOVIRALS PENTON BASE PROTEIN
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 1; Length 5; 100.0%; Pred. No. 1.9e+05;
                    Indels
                                                                                                                                                                                                                                                                APPLICANT: Kovesdi, Imre
APPLICANT: Brough, Douglas B.
APPLICANT: McVey, Duncan L.
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,162A
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Leydig, Voit & Mayer STREET: Two Prudential Plaza, Suite 4900 CITY: Chicago STATE: 111inois COUNTRY: USA
                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTRATION NUMBER: 61306
TELERHONE: (312) 616-5600
TELERHONE: (312) 616-5600
TELERHONE: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        Sequence 3, Application US/08303162A
Patent No. S558099
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
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                  5, Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Vc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
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                                                        1 EILDV 5
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                  Matches
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Sequence 10, Application US/08338282

Sequence 10, 5730978

GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ID: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
COMPUTER: Washington
COMPUTER: USA
MEDIUM TYPE: USA
MEDIUM TYPE: USA
MEDIUM TYPE: USA
MEDIUM TYPE: Windows-t
COMPUTER: Washington
COMPUTER: USA
MEDIUM TYPE: USA
MEDIUM TYPE: USA
MEDIUM TYPE: USA
MEDIUM TYPE: Windows-t
COMPUTER: WASHING SYSTEM: WS-DOS 4.01
SOFTWARE: WOY for Windows-t
CUSRENT APPLICATION DATA:
MAPLICATION NUMBER: US/08/338,282
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SOFTWARE: Patentin Releage #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
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Gaps
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Fatent No. 5962311
GENERAL INFORMATION
APPLICANT: WICKHAM, THOMAS J.
APPLICANT: ROYESDI, IMRE
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
INVENTION: USE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                  Length 5;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,846
FILING DATE: 21-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, CAROL
REGISTRATION NUMBER: 35243
REGISTRATION NUMBER: 74294
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEPHONE: (312) 616-5700
TELEPHONE: (312) 616-5700
SEQUENCE CHARACTERISTICS:
                                                                  100.0%; Score 23; DB 1; 1
100.0%; Pred. No. 1.9e+05;
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100.0%; Score 23; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
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APPLICANT: Jeffrey W. Smith
APPLICANT: Dana D. Hu
ATTLE OF INVENTION: Integrin Ligand Dissociators
FILE REFERENCE: 02046.0002
CURRENT APPLICATION NUMBER: US/09/146,503
                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09146503
Patent No. 6184206
                                    Query Match
Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-700-846-2
                                                                                                                                                                                  1 EILDV 5
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US-08-700-846-2
         US-08-709-515-3
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FILING DATE: September 1, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Sundamo,John,S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECHOMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEFAX: 1-206-224-0779
TELEEX: 4938023
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Batent No. 5731190

GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Wickham, Thomas J.
APPLICANT: McVesdi, Imre
APPLICANT: Brough, Douglas B.
APPLICANT: Brough, Douglas B.
APPLICANT: Bruder, Joseph T.
ITILE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STATE: Illinois
COMPUTER: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTARE: BREATON RElease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,515
FILING DATE: OB-SEP-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30763
REPERBINGE/DOCKET NUMBER: 30763
REQUENCE CHARACTERISTICS:
LEMOURNEY SEG ID NO: 3: SEQUENCE CHARACTERISTICS:
LEMOURNEY SEG ID NO: 3: LEMOURNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: BILDV
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-338-282-10
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Cuervo, Julio H
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO
US-08-498-237-2
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                                                                                                                                                                                                                                                           Length 5;
                                                                                                                                                                                                                                                         Query Match 100.0%; Score 23; DB 4; Length 5; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetically generated protein US-08-983-391-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lee, Wen-Cherng
APPLICANT: Lee, Wen-Cherng
APPLICANT: Hammond, Charles E.
APPLICANT: Hammond, Charles E.
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Ensinger, Carol Lee
ITILE OF INVENTION: CELL ADHESION INHIBITORS
FILE REFERENCE: 10274/024002
CURRENT PILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR PILING DATE: 1995-07-11
PRIOR FILING DATE: 1995-07-11
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
LENGTH: 5
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,463
EARLIER FILING DATE: 1997-09-03
NUMBER OF SEQ ID NOS: 3
SOFTHARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08983391
Patent No. 6239108
GENERAL INFORMATION:
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APPLICANT: Adams, Steven P.
APPLICANT: Castro, Alfredo C.
APPLICANT: Zimmerman, Craig N.
APPLICANT: Cuervo, Julio Herman
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Castro, Alfredo C
Zimmerman, Craig N
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ORGANISM: Artificial Sequence
                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                      OTHER INFORMATION: Synchetic US-09-146-503-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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APPLICANT: Les, West, Cherring
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APPLICANT: Carret, Mary B
APPLICANT: Annualst, Ronald G
APPLICANTON WROBER: ADARDED
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/376,372
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRACION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B180
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELERA: 14-8367
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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, OTHER INFORMATION: Synthetically generated peptide
US-08-875-321-2
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APPLICANT: Adams, Steven P.
APPLICANT: Lin, Ko-Chung
APPLICANT: Lin, Ko-Chung
APPLICANT: Lin, Ko-Chung
APPLICANT: Almerman, Craig N.
APPLICANT: Almerman, Craig N.
APPLICANT: Almerman, Charles B.
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Singh, Juswinder
TITLE OF INVENTION: CELL ADHESION INHIBITORS
FILE REFERENCE: 10274-023002
CURRENT APPLICATION NUMBER: US/08/875,321
CURRENT FILING DATE: 1997-09-27
PRIOR APPLICATION NUMBER: US/08/376, 372
PRIOR FILING DATE: 1995-01-23
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
IENGTH: 5
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Patent No. 6376538
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TYPE: PRT
ORGANISM: Artificial Sequence
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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RESULT 12

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GENERAL INFORMATION:
GENERAL INFORMATION:
STRUCTURAL MODELS FOR CYTOPLASHIC
TITLE OF INVENTION: DALAINS OF TRANSMEMBRANE RECEPTORS
INTERED TO STRUCTURAL MODELS FOR CYTOPLASHIC
TITLE OF INVENTION: DALAINS OF TRANSMEMBRANE RECEPTORS
INTURBER OF SEQUENCES: 20
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PAPELICATION DATA:
APPLICATION DATA:
PPLICATION NUMBER: PCT/USSS/07542
FILING DATE: 13-JUN-1994
FILING DATE: 13-JUN-1994
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: S amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
HYPOTHETICAL: NO
CREATION: Lideral
ORGANISM: Ligand sequence recognized by integrin
ORGANISM: Ligand sequence recognized by integrin
PCT-USSS-07542-3
Query Match

QUENTY MATCH

QUENTY MATCH

QUENTY MATCH

BILDV S

Db 1 EILDV S

Séarch completed: February 8, 2003, 10:30:42
JOB TIME: 15 secs
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5.1.3	Compugen Ltd.
version 5.1.3	- 2003
GenCore	(c) 1993
	Copyright

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1A-16	Gapext 0.5	283224 seqs, 96134422 residues
US-09-251-073A-16 23 1 BILDV 5	BLOSUM62 Gapop 10.0 , Gapext 0.5	283224 seqs,
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ıımum DB seq length: 0 kimum DB seq length: 200000000	Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries	.abase : PIR 73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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A;Cross-references: EMBL:X17014; NID:g453238; PIDN:CAA34878.1; PID:g40073
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Matches 5; Conserv
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A; Residues: 1-107 < KUN>
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                                                                                                                             hypothetical protein CPj0685 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: B86576
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Mycleic Asids Res 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
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A Molecule type: DNA
A Molecule type: DNA
A Cross-references: GB:AE001651; GB:AE001363; NID:g4376985; PIDN:AAD18824.1; PID:g437698
A Experimental source: strain CML029
A Genetics:
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(Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: C72047
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206666; PMID:10192388
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S13787
Conserved hypothetical protein yaak - Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Accession: S13787; S66050; C69737
R; Alonso, J.C.; Shirahige, K.; Ogasawara, N.
Nucleic Acids Res. 18, 6771-6777, 1990
A; Title: Molecular cloning, genetic characterization and DNA sequence analysis of the rA; Reference number: S13786; MUID:91088245; PMID:2124672
A; Accession: S13787
A; Retarus: preliminary
A; Residues: 1-107 < ALO>
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Matches 5; Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-50 <STO>
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R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
DNA Res. 1, 1-14, 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom A;Reference number: S65967; MUID:96051385; PMID:7584024
A;Accession: S66050
                                                                                                                                                                                                                                                                                                                A; Residues: 1.107 - OGA>
A; Rington, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
C.; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A; Britch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, i.edch, J.; Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell Y.; Authors: Lauber, J.; Capuara, A.; Oddega, B.; Rose, M.; Sediguchi, J.; Sekowska, A.; Seron, A; Authors: Schleich, S.; Schroeter, P.; Rose, M.; Sekiguchi, J.; Sekowska, A.; Seron, A; Authors: Schleich, S.; Schroeter, P.; Terpstra, P.; Tognoni, A.; Toaato, V.; Uchiyama, T.; Winters, Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Toaato, V.; Uchiyama, A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Accession: C69337
A; Accession: C69337
A; Accession: C69337
A; Accession: C69337
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C;Species: Archaeoglobus fulgidus
C;Accession: A69441
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.I
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Attle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeoglastering number: A69250; MUID:98049343; PMID:9389475
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A;Experimental source: strain 168
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ilarity 100.0%; Pred. No. 1.5e+02;
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C;Superfamily: Escherichia coli ybaB protein
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Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative 0
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15 BILDV 19
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hypothetical protein Vng1169c (imported) - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: F84272
R;Ng; W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
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Kinesin heavy chain homolog KIF5 - mouse (fragment)

Cigbecies: Mus muscallus (house mouse)

C;Bate: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998

C;Accession: C44259

R;Aizawa, H; Sekine, Y; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.

J. Cell Biol. 119, 1287-1296, 1992

A;Title: Kinesin family in murine central nervous system.

A;Reference number: A44259; MUID:93077686; PMID:1447303

A;Accession: C44259

A;Accession: C44259

A;Residues: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-143 AIZ

A;Essidues: extracted from NCBI backbone (NCBIP:118906)

C;Superfamily: kinesin heavy chain; kinesin motor domain homology

F;1-143/Domain: kinesin motor domain homology (fragment)
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A;Molecule type: DNA
A;Redidues: 1-119 <STO>
A;Cross-references: GB:AE004437; NID:g10580704; PIDN:AAG19546.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1169C
C;Superfamily: conserved hypothetical protein MJ0039
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probable PTS enzyme II B component [imported] - Escherichia coli (atrain O157:H7, substr. C;Species: Escherichia coli
C;Species: Escherichia coli O157:H7, substranta, B.; Botamousis, K.; Apodaca, Nature 409, 529-531, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Molecule type: DNA
A;Residues: 1-146 <STO>
A;Cross-references: GB:AE005174; NID:g12512844; PIDN:AAG54433.1; GSPDB:GN00145; UWGP:Z01/
A;Experimental source: strain O157:H7, substrain EDL933
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A;Experimental source: strain H37Rv
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Ayuthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Status: preliminary
A;Motacule type: DNA
A;Motacule type: DNA
A;Residues: 1-146 «HAY»
A;Cross-references: GB:BA000007; PIDN:BAB33556.1; PID:gl3359589; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80133
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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C;Superfamily: Streptomyces coelicolor hypothetical protein SC6G10.02c
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                                                                                                                                                                                                                                                                                                                    Length 146;
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; Pred. No. 1.9e+02;
0; Mismatches 0;
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C;Accession: AH0568
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servoy A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: STY0582
C;Superfamily: phosphoribosylaminoimidazole carboxylase catalytic chain; phosphoribosyla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stellate protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 19-Feb-1994 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C;Accession: S24397; S08120
R;Livak, K.J.
Genetics 124, 303-316, 1990
A;Fille: Drosophila melanogaster Stellate genes and their trans A;Reference number: S24397; MUID:90169476; PMID:1689686
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S24398
R;Livak, K.J.
Genetics 124, 303-316, 1990
A;Title: Detailed structure of the Drosophila melanogaster Stellate genes and their tran.
A;Reference number: S243997; MUID:90169476; PMID:1689686
A;Status: preliminary
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A;Cross-references: GB:AL513382; PIDN:CAD05018.1; PID:g16501801; GSPDB:GN00176
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A;Reaidues: 1-172 <LIV>
A;Cross-references: EMBL:X15899; NID:g8660; PIDN:CAA33906.1; PID:g295755
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100.0%; Score 23; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0;
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llarity 100.0%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 0;
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A;Introns: 4/2; 171/2
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Matches 5; Conservative
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                                                                                                                                                                                                                                                  Accession: Salmonella enterica subsp. enterica subsp. enterica subsp. enterica serovar Typhi
A;NOTE: this species has also been called Salmonella typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0772
C;Accession: A; Bases K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
A;Accession: AG0772
A;Status: preliminary
A;Molecule type: DNA
A;Readulues: 1-147 <PAR>A;Readulues: 1-147 <PAR>A;Genetics:
A;Genetics:
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AH0568
AH0568
Phosphoribosylaminoimidazole carboxylase catalytic chain [imported] - Salmor C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
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A;Genetic code: SGC
C;Superfamily: transcription elongation factor greb
C;Keywords: transcription factor
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Matches 5; Conserva
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17 EILDV 21
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rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A6431
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:U67548; GB:L77117; NID:g2826361; PIDN:AAB99053.1; PID:g1499895; T]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein SP1280 [imported] - Streptococcus pneumoniae (strain TIGR/
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Elsen, J.A.; Read, T.D.; Peterson, S.; Heidt on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Aluthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-180 < KUR.
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A;Experimental source: strain TIGR4
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A;Residues: 1-180 <KUR>
A;Residues: 1-180 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99961.1; PID:g15458788; GSPDB:GN00174
C;Genetics:
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llarity 100.0%; Pred. No. 2.38+02;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.4e+02;
iive 0; Mismatches 0;
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C;Superfamily: conserved hypothetical protein MJ1050
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Best Local Similarity
Matches 5; Conserv
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197114
uncharacterized conserved protein (coiled-coil) cAC1739 [imported] - Clostridium acetobu U; Species: Clostridium acetobutylicum
C; Species: Clostridium acetobutylicum
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C; Accession: P97114
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Datty, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: F97114
A; Astarture: Preliminary
                                                                                                                                                                                                                                 Aniximate kinase (EC 2.7.1.71) [imported] - Yersinia pestis (strain CO92)
C.Species: Versinia pestis
C.Species: Versinia L.Species: Versinia L.Species: Versinia L.Species: Versinia L.Species: Versinia Pestis
C.Species: Versinia L.Species: Versinia Pestis Ve
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hypothetical protein MJ1050 - Methanococcus jannaschii
c;Species: Methanococcus jannaschii
c;Species: Methanococcus jannaschii
c;Accession: A64431
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Bult, C.J.; Weich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
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A;Residues: 1-174 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79705.1; PID:g15024707; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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A;Gene: aroL
C;Superfamily: shikimate kinase; shikimate kinase homology
C;Keywords: phosphotransferase
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Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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A;Gene: CAC1739
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Cydecesion: B95321

R;Barnett, M.J; Fisher, R.F; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse Cydecesion: B95321

R;Barnett, M.J; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse Froc. Natl. Acad. Sci. U.S.A. 98, 983-9889, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilots A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Rocession: B95321

A;Status: preliminary

A;Rocession: B95321

A;Status: preliminary

A;Rocession: B95321

A;Residues: 1-217 ckUR>
A;Rocession: B95321

A;Rocession: B95321

A;Residues: 1-217 ckUR>
A;Rocession: B95321

B;Rocession: B95321

A;Rocession: B95321

B;Rocession: B95321

A;Rocession: B95321

B;Rocession: B95334; PMID:21368234; PMID:11474104

A;Rocession: B95321

B;Rocession: B95321

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nodulation protein nodB - Rhizobium meliloti (strain 41)
C;Species: Rhizobium meliloti
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
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C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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                                                                                                                                                               C;Accession: A03484
R;Torok, I.; Kondorosi, E.; Stepkowski, T.; Posfai, J.; Kondorosi, A
Nucleic Acids Res. 12, 9509-9524, 1984
A;Title: Nucleotide sequence of Rhizobium meliloti nodulation genes.
A;Reference number: A93553; MUID:85087953; PMID:6336331
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C,Species: Thermotoga maritima
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100.0%; Score 23; DB 1; I
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0;
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A;Genome: plasmid
C;Superfamily: nodulation protein nodB; nodB homology
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A;Molecule type: DNA
A;Residues: 1-217 <TOR>
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Matches 5; Conserv
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ZZZRBM
nodulation protein nodB - Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Bate: 28-May-1986 #sequence_revision 28-May-1986 #text_change 11-Apr-1997
C;Accession: A03483
R;Egelhoff, T.T.; Fisher, R.F.; Jacobs, T.W.; Mulligan, J.T.; Long, S.R.
DNA 4, 241-248, 1985
A;Title: Nucleotide sequence of Rhizobium meliloti 1021 nodulation genes: nodD is read of A;Reference number: A90951; MUD:85229955; PMID:4006668
A;Reference number: A90951; MUD:85229955; PMID:4006668
A;Accession: A03483
A;Abclecule type: DNA
A;Residues: 1-217 < AGBS
A;Cross-references: GB:X01649
A;Experimental source: strain 1021 symbiotic plasmid
C;Comment: This is one of the proteins, coded by nodulation genes, that are required for C;Genetics:
A;Genetics:
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T48130

Typothetical protein T4C9.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T48130
C;Accessio
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                                                                                                             100.0%; Score 23; DB 2; Length 180; 100.0%; Pred. No. 2.4e+02;
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A;Experimental source: cultivar Columbia; BAC clone T4C9
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Matches 5; Conservative
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EILDV 37
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A; Introns: 132/1
A; Note: T4C9.40
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          A;Gene: spr1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein AGR_L_2665 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 11-Jan-2002
C;Accession: B98297
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001708, GB:AE000512; NID:g4980740; PIDN:AAD35348.1; PID:g498075
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0260
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: C73400
R;Nolson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                     Nature 399, 323-329, 1999
Affile: Svidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Atle: Svidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Accession: C72400
A;Accession: C72400
A;Accession: preliminary
A;Actatus: preliminary
A;Actatus: Drainary
A;Residues: 1-222 <ARN>
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A,Accession: AE2586
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-231 < KUR>
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A;Molecule type: DNA
A;Residues: 1-231 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89900.1, PID:g15159849; GSPDB:GN00170
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A,Map positIon: linear chromosome
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conserved hypothetical protein MTH1192 - Methanobacterium thermoautotrophicum (strain De)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cincossion: A69026
Rismith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I gibani, D.R.; Boucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I gibani, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Jiwani, N.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct: A; Reference number: A69026
A; Reference number: A69026
A; Reference number: A69026
A; Residues: 1-242 < ARTH>
A; Reperimental source: Strain Delta H
C; Genetics:
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: 18-101-2001
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G...
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91020
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: GB:AE008689; PIDN:AAL44307.1; PID:g17741896; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont) C;Genetics: C;Genetics: Atua3494 A;Map position: linear chromosome
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A;Cross-references: GB:BA000007; PIDN:BAB36553.1; PID:g13362600; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                      Length 231;
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100.0%; Pred. No. 3.2e+02;
iive 0; Mismatches 0;
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C;Accession: Č5581
R;Lin, J.T.; Goldman, B.S.; Stewart, V.
Bacteriol. 176, 2551-2559, 1994
A;Title: The nasFEDCBA operon for nitrate and nitrite assimilation in Klebsiella pneumon A;Reference number: A55581; MUID:94222832; PMID:8169203
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C; Species: Sinorhizoblum mellioti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 17-May-2002
C; Aug-2001 #sequence_revision 24-Aug-2001 #text_change 17-May-2002
C; Aug-2001 #sequence_revision 24-Aug-2001 #text_change 17-May-2002
C; Augence M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse, Stalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizoblum melliot.)
A; Reference number: A95262; MuID: 21396509; PMID: 11481432
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Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
Abbault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.Cl
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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A;Cross-references: GB:L27431; NID:g1119218; PID:g473439
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology C;Superfamily: nucleotide binding; P-loop F;23-214/Domain: ATP-binding cassette homology <ABC>
F;23-214/Domain: ATP-binding cassette homology <ABC>
F;40-47/Region: nucleotide-binding motif A (P-loop)
A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: ONA
A;Residues: 1-25 < <OZE>
A;Cross-references: EMBL:AF038620; PIDN:AAB93487.1; GSPDB:GN00022; CESP:H10D12.2
A;Experimental source: strain Bristol N2; clone H10D12
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C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 02-Feb-2001
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A;Status: preliminary; nucleic acid sequence not shown
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
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100.0%; Score 23; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0;
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Conservative (
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A,Gene: CESP:H10D12.2
A,Map position: 4
A;Introns: 25/1; 80/1; 133/1
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Matches 5; Conserv
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C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Gpecies: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Accession: H70188
R;Fraser, C.M.; Casjens, S.; Huang, M.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Ayauthors: Smith, H.O.; Venter, J.C.
A;Althers Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70188
A;Actus: preliminary; nucleic acid sequence not shown; translation not shown
A;Mesidues: 1-253 - KLE>
A;Residues: 1-253 - KLE>
A;Experimental source: strain B31
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A, Molecule type: DNA
A, Residues: 1-250 <STO>
A, Festidues: 1-250 <STO>
A, Experimental source: GB: AE005174; NID: 912516588; PIDN: AAG57376.1; GSPDB: GN00145; UWGP: Z35
A, Experimental source: strain 0157:H7, substrain EDL933
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32649
R;Ozersky, P.
Submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid H10D12.
A;Reference number: Z21205
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Mismatches 0;
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Conservative 0
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les 5; Conserv
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            146 EILDV
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regulator of purine biosynthetic genes [imported] - Lactococcus lactis subsp. lactis (st) [Species: Lactococcus lactis subsp. lactis (c) Species: Lactococcus lactis (c) Species: Lactococcus lactis (c) Species: Lactococcus (c) Species
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R;Ohta, S.; Yohda, M.; Ishizuka, M.; Hirata, H.; Hamamoto, T.; Otawara-Hamamoto, Y.; Matrisohta, S.; Yohda, M.; Ishizuka, M.; Hirata, H.; Hamamoto, T.; Otawara-Hamamoto, Y.; Matrisochim. Biophys. Acta 933, 141-155, 1988
A;Title: Sequence and over-expression of subunits of adenosine triphosphate synthase in tA;Reference number: $01197; MUID:88163679; PMID:2894854
A;Accession: $01402
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A;Note: part of this sequence, including the amino end of the mature protein, was confirm
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C;Species: thermophilic bacterium PS-3
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Jun-2002
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R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-289 «KUR»
A, Cross-references: GB: Ab06914; PIDN: AAL03503.1; PID: g15620077; GSPDB: GN00173
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 01-Mar-2002
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; Pred. No. 3.8e+02;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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A; Residues: 1-286 <OHT>
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C64995
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C7. Special Brotein b2245 - Escherichia coli (strain K-12)
C7. Special Broterichia coli
C7. Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C7. Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C7. Accession: C64995
C7. Accession:
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                                                                                        C.Genetics:
A.Genes: SMacSs1
A.Genome: plasmid
C.Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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100.0%; Score 23; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 1 0; Indels
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C;Superfamily: erythrocyte band 7 integral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: Sulfolobus solfataricus complete genome. A; Reference number: A99139
A; Accession: H90388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 23; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 5; Conserva
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A;Molecule type: DNA
A;Residues: 1-267 <KUR>
A;Contents: annotation C;Genetics.
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D.; Roi

C, Genetics

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sulfate adenylyltransferase, chain 2 NWB1192, NWB1154 [imported] - Neisseria meningitidi:
                                                                                                                              C;Accession: B81111; B81115
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ven
A;Hitle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE002467; GB:AE002098; NID:g7226426; PIDN:AAF41575.1; PID:g7226429;
A;Experimental source: serogroup B, strain MC58
A;Accession: B81115
A;Molecule type: DNA
A;Residues: 1-307 <TE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: GB:AE002464, GB:AE002098; NID:g7226388, PIDN:AAF41540.1; PID:g7226391
A,Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: $20383; $22200
R;Chamovitz, D.; Misawa, N.; Sandmann, G.; Hirschberg, J.
FEBS Lett. 296, 305-310, 1992
A;Title: Molecular cloning and expression in Escherichia coli of a cyanobacterial gene cola; A;Reference number: $20383; MUID:92164786; PMID:1537409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Description: catalyzes the 2-step reaction from geranylgeranyl pyrophosphate (GGPP) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T41157
probable 608 acidic ribosomal protein p0 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
                                                                              C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cippecies: Symechococcus sp.
A;Variety: PCC 7942
C;Date: 19-Peb-1994 #sequence_revision 01-Mar-1996 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-307 <CHA>
A;Cross-references: EMBL:X63873; NID:g46486; PIDN:CAA45350.1; PID:g46487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Pathway: carotemoid biosynthesis
C;Superfamily: Mycobacterium marinum phytoene synthase
C;Keywords: carotemoid biosynthesis; multifunctional enzyme; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ohytoene synthase (EC 2.5.1.-) - Synechococcus sp. (strain PCC 7942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 23; DB 2; L; Pred. No. 4.4e+02; 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-307 <TET>
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244 EILDV 248
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G81905

Granda and sulfate adenylyltransferase (EC 2.7.7.4) chain 2 NWA1365 [imported] - Neisseria C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Peb-2001
C;Accession: G81905
R;Parkhill, J; Achtman, M; James, K.D; Bentley, S.D; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUD:2022556; PMID:10761919
A;Status: preliminary
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A;Residues: 1-307 <PAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84611.1; PID:g738003
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
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C;Superfamily: 3-demethylubiquinone-9 3-0-methyltransferase; bioC homology
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C;Superfamily: Caenorhabditis elegans hypothetical protein ZC13.4
                                                                                    Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 23; DB 2; Length 290; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 5; Conservative 0; Mismatches 0; Indel8
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                                                                              100.0%; Score 23; DB 2; Length 26 ilarity 100.0%; Pred. No. 4.1e+02; Conservative 0; Mismatches 0; Indels
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C;Superfamily: nodulation protein nodP
C;Keywords: nucleotidyltransferase
                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                         104 EILDV 108
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A;Residues: 1-321 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75650.1; PID:g14973054; GSPDB:GN00164; TIGR:SP46
A;Expendental source: strain TIGR4
C;Genetics:
A;Gene: SP1563
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SA0511 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #text_change 22-Oct-2001
C;Accesion: C89823
R;Kuroda, M.; Ohta, T.; Uchlyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucl ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001
Cipate: 22-Oct-2001 #sequence_revision Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Br.
Y, P.; Sun, P.M.; Winkler, M.
J. Bacteriol. D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.
J. Bacteriol. 183, 5709-5717, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A,Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A,Reference number: A97872; MUID:21429245; PMID:11544234
A,Accession: D98049
A,Accession: D98049
A,Residues: L-322 < kUR>
A,Residues: 1-322 < kUR>
A,Cross-references: GB:AE007317; PIDN:AAL00225.1; PID:g15459075; GSPDB:GN00174
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A;Molecule type: DNA
A;Residues: 1-21 <KUNA
A;Cross-references: GB:BA000018; PID:g13700444; PIDN:BAB41742.1; GSPDB:GN00149
A;Experimental source: strain N315
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C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
C;Keywords: oxidoreductase
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100.0%; Score 23; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0;
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Lranscription antitermination factor nueg - Mycoplasma pneumoniae (strain ATCC 29342)

N.Alternate names: hypothetical protein D09_orf320

C;Species: Mycoplasma pneumoniae

A;Variety: ATCC 29342

C;Date: 26-Fb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C;Accession: S73413

R;Himmelreich, R:; Hilbert, H; Plagens, H:; Pirkl, E:; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Retus: preliminary; nucleic acid sequence not shown; translation not shown

A;Rosalues: 1-20 < HIM.

A;Rosa-references: EMBL.AE000011; GB:U00089; NID:g1673740; PIDN:AAB95735.1; PID:g167374

A;Rosa-references: EMBL.AE000011; GB:U00089; NID:g1673740; PIDN:AAB95735.1; PID:g167374

A;Genetics: A;Genetics:
A;Genetic code: SGC3
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A95182
Cypothetical protein SP1563 [imported] - Streptococcus pneumoniae (strain TIGR4)
Cypothetical protein SP1563 [imported] - Streptococcus pneumoniae
Cypothetical protein SP1563
Cypothetical protein SP1563
Cypothetical protein SP1582
Cypothetical Protein SP182
Rytetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Accession: A95182
A;Accession: A95182
A;Accession: A95182
A;Molecule type: DNA
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 C;Accession: T41157 R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Bubmitted to the EMBL Data Library, October 1998 A;Reference number: Z21973 A;Recession: T41157 A;Accession: T41157 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: DNA A;Residues: 1-312 *AILL.
A;Cross-references: EMBL:AL031907; PIDN:CAA21428:1; GSPDB:GN00068; SPDB:SPCC18.14c A;Experimental source: strain 972h-; cosmid c18
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C;Superfamily: rat acidic ribosomal protein P0
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64665
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Redidues: preliminary; nucleic acid sequence not shown; translation not shown A;Redidues: 1-324 crOM>
A;Cross-references: GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD08209.1; PID:g2314321
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C;Superfamily: phosphoribosylformylglycinamidine cyclo-ligase; phosphoribosylformylglycir
F;6-326/Domain: phosphoribosylformylglycinamidine cyclo-ligase homology <PFCL>
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R.Stone, E.M.; Yamano, H.; Kinoshita, N.; Yanagida, M.
Curr. Biol. 3, 13-26, 1993
A.Pitle: Mitchic regulation of protein phosphatases by the fission yeast sds22 protein. A.Feference number: S43988
A.Pitle: Mitchic compared with conceptual translation
A.Molecule type: DNA
A.Residues: 1-33 csTO>
R.Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Sybelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
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A;Experimental source: strain 972h-; cosmid c4A8
R;Ohkura, H.; Yanagida, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Species: Archaeoglobus fulgidus
C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
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A;Molecule type: DNA
A;Residues: 1-332 <SKE>
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A;Accession: T38782
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Matches 5, Conser
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C;Species Helicobacter pylori

A;Variety: strain J99)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C;Date: 12-Feb-199
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A;Experimental source: strain J99
C;Genetics:
A;Gene: trxB_2
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: D64665
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T36941
R;Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.submitted to the EMBL Data Library, September 1999
A;Reference number: Z21607
A;Accession: T36941
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A, Residues: 1-322 <SEE>
A, Cross-references: EMBL.AL109962; PIDN:CAB53126.1; GSPDB:GN00070; SCOEDB:SCJ1.08
B, Experimental source: strain A3(2)
C, Genetics:
A, Gene: SCOEDB:SCJ1.08
C, Keywords: transcription initiation
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100.0%; Score 23; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0;
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Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative 0
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A; Residues: 1-338 < KAT>
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                                                                                                                                                                           212 EILDV 216
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C; Species: Nostoc sp.
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: Ap2079
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sp. 750-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AB2079
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-337 «KUR»
A; Rosis-references: GB:BA000019; PIDN:BAB73886.1; PID:g17131278; GSPDB:GN00179
A; Experimental source: strain PCC 7120
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C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82910
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A8297
A;Accession: A8297
A;Status: preliminary
A;Rotatus: DNA
A;Rotatus: DNA
A;Rotatus: DNA
A;Rotatus: DNA
A;Coss-references: GB:AE002107; GB:AF222894; NID:g6899022; PIDN:AAF30482.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
Cell 64, 149-157, 1991
A;Title: Schizosaccharcmyces pombe gene sds22+ essential for a midmitotic transition end A;Atle: Schizosaccharcmyces pombe gene sds22+ essential for a midmitotic transition end A;Accession: A38439; MUID:91098642; PMID:1846086
A;Accession: A38439
A;Status: preliminary
A;Actus: preliminary
A;Residues: 53-332 < CHK>
A;Access-references: GB:M57495; NID:9173478; PIDN:AAA35342.1; PID:9173479
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A;Introns: 41/3
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
C;Keywords: nucleus
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Best Local Similarity 100.
Matches 5; Conservative
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A;Gene: sds22; SPAC4A8.12c
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A,Gene: UU077
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aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - Shewanella sp. DSS12
N;Alternate names: aspartate beta-D-semialdehyde dehydrogenase
C;Species: Shewanella sp. DSS12
C;Date: 17-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C;Accession: JC5436
E;Kato, C.; Smorawinska, M.; Li, L.; Horikoshi, K.
J. Biochem. 121, 717-723, 1997
A;Title: Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenasr
A;Reference number: JC5435; MUID:97306055; PMID:9163523
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R;Kato, C.; Smorawinska, M.; Li, L.; Horikoshi, K.
B.;Chem. 121, 717-723, 1997
A;Title: Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenas A;Reference number: JC5435; MUID:97306055; PMID:9163523
A;Accession: JC5435
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A;Experimental source: strain DSS12
C;Comment: This enzyme is a key enzyme in the biosynthetic pathway of lysine, threonine,
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A;Experimental source: strain DB6705
C;Comment: This enzyme is a key enzyme in the biosynthetic pathway of lysine, threonine,
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100.0%; Score 23; DB 2; L
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0;
Score 23; DB 2; I Pred. No. 4.9e+02; 0; Mismatches 0;
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C,Superfamily: aspartate-semialdehyde dehydrogenase
C,Keywords: oxidoreductase
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J. Biol. Chem. 263, 12109-12114, 1988
A;Title: Transcriptional Organization of the dnaN and recF Genes of Escherichia coli K-1;
A;Reference number: I41190; MUID:8829898; PMID:2841344
A;Accession: I41190
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A;Title: Overlapping arrangement of the recF and dnaN operons of Escherichia coli; Positi
A;Reference number: 154000; MUID:86301872; PMID:3527871
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 194000
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Acces-references: 143-170
A;Esaiduse: 143-170
A;Ases-references: GB:M13822; NID:g147541; PIDN:AAA24512.1; PID:g147542
A;Cross-references: GB:M13822; NID:g147541; PIDN:AAA24512.1; PID:g147542
A;Rose-references: GB:M13822; NID:g147541; PIDN:AAA24512.1; Burland, V.; Riley, M.; Co:A; Rose-reference 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB: K02179; NID: g147537; PIDN: AAA24510.1; PID: g147538
R; Adachi, T.; Mizuuchi, K.; Menzel, R.; Gellert, M.
R; Adachi, T.; Mizuuchi, K.; Menzel, R.; Gellert, M.
A; Dritle: DNA sequence and transcription of the region upstream of the E. coli gyrB gene.
A; Reference number: A22168; MUID: 84297235; PMID: 6089112
A; Accession: A22168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Escherichia coli (strain K-12)
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rosidues: 1-357 <CW1
A,Rosidues: 1-357 <CW1
A,Cross-references: EMBL.AL031603; PIDN:CAA20909.1; GSPDB:GN00068; SPDB:SPCC330.04c
A,Experimental source: strain 972h-; cosmid c330
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,Molecule type: DNA
,Residues: 342-366 <ADA>
,Cross-references: GB:X04341, GB:X00870, NID:g41643; PIDN:CAA27869.1; PID:g41644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Escherichia coli
C;Date: 28-Aug-1985 #sequence revision 31-Mar-1988 #text change 01-Mar-2002
C;Accession: A91510; A93996; Ā22168; I41190; I54000; F65Ī72; A00719; B24944
R;Ohmori, H.; Kimura, M.; Nagata, T.; Sakakibara, Y.
Gene 28, 159-170, 1984
A;Title: Structural analysis of the dnaA and dnaN genes of Escherichia coli.
A;Reference number: A91510; MUID:84237568; PMID:6234204
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                                                                                                                                                                                                                                                       A;Gene: SPDB:SPCC330.04c
A;Map position: 3
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Matches 5; Conserv
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A; Molecule type: DNA
A; Residues: 1-366 < OHM>
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A;Molecule type: DNA
A;Residues: 1-14 <RES>
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Honolog - Lywe disease spirochete
C; Species: Borrelia burgdorferi (Lywe disease spirochete
C; Species: Borrelia burgdorferi (Lywe disease spirochete)
C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 26-Aug-1999
C; Accession: B70136
C; Accession: B70136
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lywe disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685
A; Reference number: A70100; MUID:98065943; PMID:9403685
A; Accession: B70136
A; Accession: B70136
A; Relatus: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-344 *KLE>
A; Cross-references: GB:AE001137; GB:AE000783; NID:92688160; PIDN:AAC66658.1; PID:9268817
A; Experimental source: strain B31
C; Superfamily: flagellar switch protein flig
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C;Species: Homosappens (man)
C;Species: Homosappens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000
C;Caccession: 23508; Anderton, B.H.
Biochem. J. 284, 469-476, 1992
A;Title: Human homologues of the bacterial heat-shock protein DnaJ are preferentially ex A;Title: Human homologues of the bacterial heat-shock protein DnaJ are preferentially ex A;Status: preliminary
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-351 cCHE>
A;Cross-references: BMB:X63368; NID:g32468; PIDN:CAA44968.1; PID:g32469
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hypothetical repeat-containing protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 0.3-Dec-1999 #sequence_revision 0.3-Dec-1999 #text_change 0.3-Dec-1999
C;Accession: T41314
R;Gwilliam, R.; Barrell, B.G.; Rajandream, M.A.; Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21987
A;Accession: T41314
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-274, 'DVF' < CH2>
A; Cross-references: EMBL:X63368; NID:g32468; PIDN:CAA44969.1; PID:g32470
C; Genetics: 2;
A; Introns: 275/1
C; Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;3-69/Domain: dnaJ amino-terminal homology
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Best Local Similarity 100.0°
Matches 5; Conservative
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8 EILDV 12
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A;Molecule type: DNA
A;Residues: 1-366 <KUR>
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D91208
DNA polymerase III beta-subunit [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C; Accession: D91208
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-366 < HNX>
A; Residues: 1-366 < HNX>
A; Excession: D91208
A; Cross-references: GB:BA000007; PIDN:BAB38059.1; PID:g13364111; GSPDB:GN00154
A; Excession: Bource: strain O157:H7, substrain RIMD 0509952
RESULT 62
F86054
PNDA polypmerase III, beta-subunit [imported] - Escherichia coli (strain 0157:H7, substrai C;Species: Escherichia coli errain 0157:H7, substrai C;Species: Escherichia coli ervision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: F86054
Fyerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                           te; the holoenzyme is completed by where the holoenzyme is completed by which the holoenzyme is completed for initiation of replication
A; Description: beta chain is required for initiation of replication
A; Note: can slide along duplex DNA bidirectionally and ATP-independent; binds core; cryst c; Superfamily: DNA-directed DNA polymerase III beta chain
C; Superfamily: DNA replication initiation; nucleotidyltransferase
C; Keywords: DNA replication initiation; nucleotidyltransferase
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A;Gene: ECG4636
C;Superfamily: DNA-directed DNA polymerase III beta chain
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A;Status: preliminary
A;Molecule type: DNA
C;Superfamily: DNA-directed DNA polymerase III beta chain
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Nature 413, 846-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Accession: AB0958
A;Accession: AB0958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <PRA>
A;Residues: 1-366 <PRA>
A;Cross-references: GB:AL513382; PIDN:CAD03158.1; PID:g16504793; GSPDB:GN00176
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C;Species: Yersinia pestis
C;Date: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AF0497
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., R;Parkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Invarue 413, 523-527, 2001
Nature 413, 523-527, 2001
A;Fitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB0958
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 23; DB 2; Length 366; Best Local Similarity 100.0%; Pred. No. 5.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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Query Match 100. Best Local Similarity 100. Matches 5; Conservative

304 EILDV 308

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1 EILDV

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high affinity transport system protein P37 - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: hypothetical protein A05_orf380V
C;Species: Mycoplasma pneumoniae
A;Variety. ATCC 29342
C;Date: 10-Sep-1999 #text_change 10-Dec-1999
C;Accession: S73751
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Angle Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-directed RNA polymerase, subunit A' (rpoA2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: H69485
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
T; Fleischmann, R.D.; Quackehbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A,Athohors: Utchaebck, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeori
A;Refearence number: A69250; MUID:98049343; PMID:9389475
A;Refearence number: A69250; MUID:98049343; PMID:9389475
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 cKLE>
A;Cross-references: GB:AE000972; GB:AE000782; NID:g2689295; PIDN:AAB89364.1; PID:g2648655; C;Superfamily: DNA-directed RNA polymerase II
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 0.5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: B70076
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc C.; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho. M.; Entich, S.D.; Emmerson, P.T.; Entian, K.D.; Brrington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerciech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: S73751
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-380 «HIM»
A,Cross-references: EMBL:AE000041; GB:U00089; NID:g1674104; PIDN:AAB96073.1; PID:g167411
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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A,Genetic code: SGC3
A,Start codon: GTG
C,Superfamily: Mycoplasma hyorhinis high affinity transport system protein P37
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100.0%; Score 23; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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100.0%; Score 23; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                               RESULT 65
H97386
periplasmic mannitol-binding protein, smoM (AF018073) [imported] - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: H97388
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
A;Accession: H97388
A;Accession: H97388
A;Accession: H97389
A;Cross-references: GB:AE007869; PIDN:AAK86065.1; PID:g15155140; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C 426
A;Map position: circular chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aftite: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8. A;Reference number: AB2577; FMID:11743193
A;Accession: A12606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41271.1; PID:g17738578; GSPDB:GN00186
C;Genetics:
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                Length 366;
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        100.0%; Score 23; DB 2; Length 36
100.0%; Pred. No. 5.3e+02;
ive 0; Mismatches 0; Indels
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100.0%; Score 23; DB 2; I
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0;
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306 EILDV 310

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A; Map position: circular chromosome

A; Gene: Atu0249

306 EILDV 310 1 EILDV S

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RESULT 67 S73751

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185 EILDV 189
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A;Accession: H72323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-386 <ARN>
A;Residues: 1-386 <ARN>
A;Cross-references: GB:AE001753; GB:AE000512; NID:g4981397; PIDN:AAD35959.1; PID:g498141
A;Experimental source: strain MSB8
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle A.; R.; Ogiwar, K.; Sroche, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A.; Authors: Voshikawa, H.; Danchin, A.; Tosato, V.; Voshida, K.; Authors: Voshikawa, H.; Danchin, A.; Astatus, R.; Yoshikawa, H.; Danchin, A.; Astatus, R.; Ayatehors: Assersiminary; nucleic acid sequence not shown; translation not shown
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B70302
C) Depoison cofactor biosynthesis protein A - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E70302
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ox
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C;Superfamily: Helicobacter pylori 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid ferred
C;Keywords: oxidoreductase
F;8-189/Domain: 2-oxoacid ferredoxin oxidoreductase homology <FEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2-oxoglutarate-ferredoxin oxidoreductase (BC 1.2.7.-) alpha chain TM0878 [similarity] - C;Species: Thermotoga maritima C;Species: Thermotoga maritima C;Oate: Il-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: H72323 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:299124; GB:AL009126; NID:g2636442; PIDN:CAB15983.1; PID:g2636493
A;Experimental source: strain 168
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Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID;9537320
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A,Gene: yxeP
C,Superfamily: hippurate hydrolase
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1es 5, Conservative
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-380 <KUN>
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44 EILDV 48
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A;Residues: 11402 <AQF>
A;Cross-references: GB:AE000670; GB:AE000657; NID:g2982779; PIDN:AAC06407.1; PID:g298278;
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C;Accession: T04821
R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, Hankeference number: Z15385
A;Reference number: Z15385
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C;Species Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: E71087
C;Accession: E71087
C;Accession: F1087
M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekinc M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic as A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
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A;Accession: E70302
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0041
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A;Residues: 1-407 <KAW>
A;Cross-references: GB:AP000004; NID:93236131; PIDN:BAA30059.1; PID:93257376
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A;Introns: 68/1; 110/3; 176/2; 195/2; 221/2; 269/3
A;Note: F10M23.320
C;Superfamily: Arabidopsis thaliana hypothetical protein F10M23.320
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Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                            A;Gene: moeAl
C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2
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A;Reaidues: 1-403 <BEV>
A;Cross-references: EMBL:AL035440
A;Experimental source: cultivar Columbia; BAC clone F10M23
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Search completed: February 8, 2003, 10:25:02
Job time : 21 secs
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: G4-Dec-1986 #Bequence_revision 05-Dec-1997 #text_change 01-Mar-2002
C;Accession: H64748; A04451
R;Blattner, F.R; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
C;Accession: H64748 B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64748
A;Retaus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-414 <-BLAT>
A;Ross-references: GB:AE000132; GB:U00096; NID:92367098; PIDN:AAC73343.1; PID:91786434;
A;Reperimental source: strain K-12, substrain MG1655
B;Nusser, J. Schumperli, D.
Gene 32, 243-249, 1994
A;Title: Structural and functional organization of the gpt gene region of Escherichia cc
A;Accession: A4448
                                                                                                                                                                                                                    Syferal protein - Synechocystis sp. (strain PCC 6803)

hypothetical protein - Synechocystis sp.
(sSpecies Synechocystis sp.
4;Variety: PCC 6803)

C;Species: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S76678

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A,Residues: 1-241,'S',243-276,'TL',279-396,'KILTKVFRKSPTGS',411,'NA',414,'VKNLLNFANLVKQL
A,Cross-references: GB:M1342; NID:g146255; PIDN:AAA23929.1; PID:g146257
C,Comment: The gene coding for this protein is located between the gpt and phoE genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S74322; MUID: 97061201; PMID: 8905231
A; Accession: S76678
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-408 < KAN>
A; Residues: 1-408 < KAN>
A; Cross-references: EMBL: D64004; GB: AB001339; NID: 91001701; PIDN: BAA10622.1; PID: 9120845
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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100.0%; Score 23; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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C,Superfamily: yafA protein
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                                                                    389 EILDV 393
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1 EILDV 5
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

; Search time 11 Seconds (without alignments) 18.853 Million cell updates/sec 8, 2003, 10:20:02 February Run on:

US-09-251-073A-16 23 Title: Perfect score:

1 EILDV 5 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

82 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

length: 0 length: 2000000000 sed

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries

SwissProt_40:* Оатараве : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

P24281 bacillus su 03446 wolinella si 99947 ureaplasma P15021 drosophila 658450 methanococc 004663 arabidopsis P02063 rhizobium m P58154 lymnaea sta 099715 mus musculu P76469 escherichia P76469 escherilus ps P91010 bacillus sta P41010 bacillus sta P42007 bacillus sta P420 clostridium borrelia bu homo sapien archaeoglob escherichia bacillus su serine/th homo sapien escherichia salmonella mycoplasma Description Q61151 Q16739 P04335 P37722 P26464 P75371 P26836 P25686 P00583 028390 P54955 ACHP_LYMST DJBA_MOUSE NASD_KLEPN YFAU_ECOLI PURR_LACLA ATPG BACCA ATPG BACST UBIG RICCN CRTB SYNP7 Y054 MYCPN SD22 SCHPO DHAS SHESP DHAS SHEVI LYC CLOPE FLIG BORBU DJB2 HUMAN DP3B ECOLI DP3B SALTY P37 MYCPN RPAZ ARCFU YXEP BACSU 2ASE MOUSE YAAK BACSU PAND WOLSU GREA UREPA STEL DROME YASO METJA IFE2 ARATH NODB RHIME SALTY BACP3 HUMAN ATPG Query Match Length DB 100.0 100.0 100.0 100.0 0.001 . 00 8 Score Result Š

	087924 pseudomonas Q9rers deinococcus Q28275 canis famil Q28377 equus cabal Q12836 h serine/th Q28651 o serine/th Q92959 chlamydia p Q26653 o serine/th Q14738 h serine/th Q14738 h serine/th Q14738 h serine/th			P7334 synechocyst Q9hmx8 halobacteri Q02357 mus musculu P16157 homo sapien P07589 bos taurus P02751 homo sapien P11276 mus musculu P04337 zattus norv Q91740 xenopus lae
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33 3 3 3 3 4 4 4 4 9 9 9 9 4 1 1 1 1 1 1 1 1 1 1 1	4 4 4 4 4 4 4 4 10 10 10 10 10 10 10 10 10 10 10 10 10	. 4 N N C B O O O C C C C C C C C C C C C C C C	4 7 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 C C C C C C C C C C C C C C C C C C C

ALIGNMENTS

SEQUENCE FROM N.A.
MEDLINE=91088245; PubMed=2124672;
Alonso C., Shirahige K., Ogasawara N.;
"Molecular cloning, genetic characterization and DNA sequence analysis of the reckn region of Bacillus subtilis.";
Nucleic Acids Res. 18:6771-6777(1990). Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus. NCBI_TaxID=1423; (Rel. 21, Created) (Rel. 21, Last sequence update) (Rel. 41, Last annotation update) 107 AA PRT; 01-MAR-1992 (Rel. 21, Cree 01-MAR-1992 (Rel. 21, Last 15-JUN-2002 (Rel. 41, Last Hypothetical protein yaak STANDARD; Bacillus subtilis. YAAK BACSU P24281; RESULT 1 YAAK BACSU YAAK

salmonella

AFA

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     Gross R., Simon J., Theis F., Kroeger A.;
"Two membrane anchors of Wolinella succinogenes hydrogenase and their
"Two membrane anchors of Wolinella succinogenes hydrogenase and their
function in fumarate and polysulfide respiration.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-aspartate = beta-alanine + CO(2).
-!- CATALYTIC ACTIVITY: L-aspartate = beta-alanine + CO(2).
-!- PATHWAY: Pantothenate biosynthesis; second branch.
-!- SIMILARITY: BELONGS TO THE PAND FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASPARTATE 1-DECARBOXYLASE ALPHA CHAIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASPARTATE 1-DECARBOXYLASE BETA CHAIN (BY SIMILARITY).
                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aspartate 1-decarboxylase precursor (EC 4.1.1.11) (Aspartate alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pantothenate biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen.
                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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116-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Transcription elongation factor greA (Transcript cleavage factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
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CONVERTED TO A PYRUVOYL GROUP (BY
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; 41FB7B63B571F837 CRC64;
                                                         121 AA
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Pfam; PF02261; Asp decarbox; 1.
TIGRFAMS; TIGR00223; panD; 1.
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                                                         STANDARD;
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                                                                                                                                                                                                                                                               Wolinella succinogenes.
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                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=844;
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                                                                                                                                                                                                                 decarboxylase).
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Q9PQI7;
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                                                      PAND WOLSU
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                                                                                 034246;
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GREA_UREPA
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                                                                                                                                                                                                                                                                          Muster F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Bartise R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capusno V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Bronizof F., Devine K.M., Dusterhoft A., Erhilch S.D., Ramerson P.T.,

Bartian K.D., Brrington J., Febret C., Ferrari E., Foulger D.,

Rritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

A Glims S.Y., Claser P., Ocffeau A., Golightly E.J., Grandi G.,

A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

A Kuita K., Lapidus A., Lardinois S., Lauber J., Lazareric V.,

A Kuita K., Lapidus A., Lardinois S., Lauber J., Lazareric V.,

Ra Kobayashi Y., Koetter P., Mizuno M., Moestl D., Nakai S., Noback M.,

Randina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

Randon D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

Rarko V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

Rarko T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

A Toscohi B., Tamaka T., Takahashi H., Takemaru K.,

Takeuchi M., Tamakoshi A., Tanaka T., Tarahashi H., Takemaru K.,

Takeuchi M., Tamakoshi A., Tanaka T., Tarahashi H., Wanbut K.,

Yaari A., Wambutt R., Wadler E., Wedler E., Wedl
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                                                                            Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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11781 MW; DB3EBA3420F6A9E6 CRC64;
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100.0%; Pred. No. 51;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390:249-256(1997).
-!- SIMILARITY: BELONGS TO THE UPF0133 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGREAMS; TIGR00103; Cons hypoth103; 1.
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InterPro; IPR004401; Cons hypoth103.
InterPro; IPR003727; DUF149.
                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                                   MEDLINE=96051385; PubMed=7584024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X17014; CAA34878.1; -. EMBL; D26185; BAA05256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z99104; CAB11796.1; -. PIR; S13787; S13787.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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107 AA; 11
                                                                                                                                                             DNA Res. 1:1-14(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
SEQUENCE FROM N.A.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
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                                                                                                                                                                                                                                         STRAIN=168;
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Gaps

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SEQUENCE FROM N.A. STRAIN-Serovar 3;

EILDV 56

25

Matches

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-!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
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    MARKAR RANGE OF THE PARTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation, DNA-binding, Coiled coil, Complete proteome.

7 24 COILED COIL (POTENTIAL).

DOMAIN 42 84 COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics 124:303-316(1990).

-!- FUNCTION: RESPONSIBLE FOR THE APPEARANCE OF PROTEINACEOUS STAR-SHAPED CRYSTALS IN THE PRIMARY SPERMATOCYTES OF D.MELANOGASTER MALES LACKING A Y CHROMOSOME.

-!- MISCELLANEOUS: THERE ARE MULTIPLE COPIES OF THE STELLATE GENE IN FRUIT FLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Perygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227,
                                                                                                                          LIF 407.7597-762 (2000).

FUNCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION ELONGATION PAST TEMPLATE-ENCODED ARRESTING SITES. THE ARRESTING SITES IN DNA HAVE THE PROPERTY OF TRAPPING A CERTAIN FRACTION OF ELONGATING RNA POLYMERASES THAT PASS THROUGH, RESULTING IN LOCKED TERNARY COMPLEXES. CLEAVAGE OF THE NASCENT TRANSCRIPT BY CLEAVAGE FACTORS SUCH AS GREA OR GREB ALLOWS THE RESUMPTION OF ELONGATION FROM THE NEW 3'TERMINUS. GREA RELEASES SEQUENCES OF 2 TO 3 NUCLEOTIDES (BY SIMILARITY).
                  Glass J. I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H., "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P21346; 1GRJ; GreA GreB.
InterPro; IPR001437; GreA GreB.
Pfam; PF0127; GreA GreB; 1.
Pfam; PF03449; GreA_GreB_N; 1.
Propon; PD004918; GreA GreB; 1.
PROSITE; PS00829; GREAB_1; 1.
PROSITE; PS00830; GREAB_2; FALSE_NEG.
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STRAIN=Oregon-R; TISSUE=Testis;
MEDLINE=90169476; PubMed=1689686;
MEDLINE=20500219; PubMed=11048724;
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                                                                                                              Nature 407:757-762(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcripts.";
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01-APR-1990
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P15021;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 1; Length 172; 100.0%; Pred. No. 85; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Testis; Multigene famīly.
SEQUENCE 172 AA; 19507 MW; C86304F591E76F8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea, Buryarchaeota, Methanococci; Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
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Pfam; PF01121; CoaB; 1.
Hypothetical protein; ATP-binding; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                entities requires a license agreement (Se
or send an email to license@lsb-sib.ch).
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AL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                     Flybase; FBgn0003523; Ste.
InterPro; IPR000704; CAS Kinase_II.
Pfam; PF01214; CK II beta; 1.
PRINTS; PR00472; CASWKINASEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01101; CK2 BETA; 1.
                                                                                                                                                                                                                                                                                                                  EMBL; X15899; CAA33906.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
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PIR; S24397; S24397
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PURCTION: RECOGNIZES AND BINDS THE 7-METHYLGUANOSINE-CONTAINING MRNA "CAP" DURING AN EARLY STEP IN THE INITIATION OF PROTEIN SYNTHESIS AND FACILITARES RIBOSOME BINDING BY INDUCING THE UNMINDING OF THE MRNAS SECONDARY STRUCTURES (BY SIMILARITY). SUBBUNIT: EIFAF IS A TRIMER COMPOSED OF BIF4E, EIFAFG AND EIFAFA (WHICH CAN CYCLE IN AND OUT OF THE COMPLEX). IN HIGHER PLANTS TWO ISOPRING OF EIFAFF HAVE BEEN IDENTIFIED, NAMED EIFAF AND EIF(ISO) 4F. EIFAFF HAS SUBUNITS P220 AND P28, WHEREAS EIF-(ISO) 4F HAS SUBUNITS P82 AND P28 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                  Gaps
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MEDLINE=98403884; PubMed=9734815;
Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wittmann S., Charel H., Fortin M.G., Laliberte J.F., Interaction of the viral protein genome linked of turnip mosaic potyvirus with the translational eukaryotic initiation factor (iso) 4E of Arabidopsis thallana using the yeast two-hybrid system.";
                                                                                                                                                                                                                                                                                                                                    014653; OSSANS; 15-JUL-1998 (Rel. 36, Created) 16-JUL-1998 (Rel. 36, Created) 16-OCT-2010 (Rel. 40, Last sequence update) 16-OCT-2010 (Rel. 40, Last amnotation update) Eukaryotic translation initiation factor 4E (eIF-4E) (eIF4E) (mRNA cap-binding protein) (eIF-(iso)4F 25 KDa subunit) (eIF-(ISO)4F P28 subunit) (eIF4E2 OR AT5G35620 OR WJE4.8. Arabidopsis thaliana (Mouse-ear cress).
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                                                                  Length 177;
                                                                                                                  Indels
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
14 ATP (POTENTIAL).
20690 MW; F209572AA79CD2F9 CRC64;
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                                                                     DB 1;
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                                                                                          88;
                                                                100.0%; Score 23; DE
100.0%; Pred. No. 88;
tive 0; Mismatches
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MEDLINE=97378268; Pubmed=9234949;
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                                                                                        Local Similarity 100.
1es 5; Conservative
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                   177 AA;
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NP_BIND
SEQUENCE
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HSSP;
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Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federapiel N.A., Long S.R.;
"Nuclectide sequence and predicted functions of the entire
Sinorhizobium meliloti psym Amegaplasmid.",
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001)
-!- FUNCTION IS INVOLVED IN GENERALING A SMALL HEAT-STABLE COMPOUND
(NOD), AN ACYLATED OLIGOMER OF N-ACETYLGLUCOSAMINE, THAT
STIMULATES MITOSIS IN VARIOUS PLANT PROTOPLASTS.
                                                                                                                                                                                                                                                                                                                                      Gaps
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Nucleic Acids Res. 12:9509-9524(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Pred. No. 99;
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"The complete sequence of S. meliloti 042B nodABC.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         198 AA; 22514 MW; 71FEB309E073A9D2 CRC64;
InterPro; IPR001040; TIF_eIF_4E.

PEam; PP01652; IF4E; 1.

ProDom; PD003697; TIF_eIF_4E; 1.

PROSITE; PS00813; IF4E; 1.

PRICIATION factor; Protein biosynthesis; RNA-binding; Multigene family.

SEQUENCE 198 AA; 22514 MW; 71FEB309E073A9D2 CRC64.
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-!- SIMILARITY: TO OTHER POLYSACCHARIDE DEACETYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P02963; 052477;
21-UL-1986 (Rel. 01, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Chitooligosaccharide deacetylase (EC 3.5.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NODB OR RA0474 OR SMA0868.
Rhizobium meliloti (Sinorhizobium meliloti).
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                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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MEDLINE=21396509; PubMed=11481432;
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MEDLINE=85229955; PubMed=4006668;
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Best Local Similarity
'-haq 5; Conserve
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Q9QYIS;
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DISULFID
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch)
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"A glia-derived acetylcholine-binding protein that modulates synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Acetylcholine-binding protein precursor (ACh-binding protein) (AchBP)
Lymnaea stagnalis (Great pond snail).
Elwaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Lymnaeidae; Lymnaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASS SPECTROMETRY: MW-24720.4; METHOD=GTOF; RANGE=20-229.
SIMILARITY: TO THE EXTRACELLULAR PORTION OF LIGAND-GATED IONIC
CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 20-229.
MEDLINE=21256199; PubMed=11357122;
MEDLINE=21256199; PubMed=11357122;
Van Der Oost J., Smit A.B., Sixma T.K.;
"Crystal structure of an ACh-binding protein reveals the ligand-binding domain of nicotinic receptors.";
Nature 411:269-276(2011).
I- FUNCTION: BINDS TO ACETYLCHOLINE. MODULATES NEURONAL SYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMISSION.
SUBUNT: HOWOPENTAMER.
SUBCELLULAR LOCATION: SECRETED. RELEASED IN AN ACETYLCHOLINE-DEPENDENT MANNER. IN THE SYNAPTIC CLEFT.
TISSUE SPECTFICITY: EXPRESSED BY GLIAL, CELLS.
PTM: N-GLYCOSYLATED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 411:261-268(2001).
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P58154;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 N-LINKED (GLCNAC. .) (PROBABLE)
26061 MW; B76A3A13E7EF8FCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 1; Length 229;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                           ACETYLCHOLINE-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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28601 MW; 81387B09ADF9B09A CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DnaJ homolog subfamily B member 10 (mDJ8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                           or send an email to license@isb-sib.ch).
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PROSITE; PS50076; DNAJ_2; 1.
                                                                                                                                                                                                                                                                                                                                                         3D-structure.
                                                                                                                                                                                                         EMBL; AF364899; AAK64377.1; -.
PDB; 119B; 16-MAY-01.
InterPro; IPR001175; Neur channel.
PEm; PF02931; Neur chan_IBD; 1.
Glycoprotein; Signal; 3D-structure.
SIGNAL
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Ohtsuka K., Hata M.;
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InterPro; IPR002950; Josephin.
InterPro; IPR003903; UIM.
Pfam; PP00226; DnaJ; I.
Pfam; PP02909; UIM; 2.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY PART OF A HIGH-AFFINITY BINDING-PROTEIN-
DEPENDENT TRANSPORT SYSTEM FOR NITRATE. PROBABLY RESPONSIBLE FOR
BNERGY COUPLING TO THE TRANSPORT SYSTEM.
-!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                    Gaps
                                                                                                                                                                                                                   Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella.
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                                                                                                                                                                                                                                                                                                MEDLINE=94222832; PubMed=8169203;
Lin J.T., Goldman B.S., Stewart V.;
"The nasFBDCBA operon for nitrate and nitrite assimilation in
Klebsiella pneumoniae MSal.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 1; Length 262; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
             Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L27431; AAB86901.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003493; ABC_transportr.
Pfam; PP00005; ABC_tran; 1.
ProDom; PD00006; ABC_transportr; 1.
SMART; SM00382; AAA; 1.
TIGRPAMs; TIGRPAMs; TIGRD1184; LTCD; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
TRANSPORT; ATP-binding; Membrane; Nitrate assimilation.
NP BIND 4TP (POTENTIAL).
SEQUENCE 262 AA; 28996 MW; AD1B32490A2AEA10 CRC64;
                                  0; Indels
             100.0%; Score 23; DB 1; I
100.0%; Pred. No. 1.3e+02;
                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
15-2011-1998 (Rel. 36, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Nitrate transport protein nasD.
                                                                                                                                        262 AA
                                   0; Mismatches
                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                Bacteriol. 176:2551-2559(1994).
Query Match
Best Local Similarity 100...
Si Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=573;
                                                                               6 EILDV 10
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                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=M5a1;
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                                                                                                                                                                                                                                                                                                                                                                                             Stewart V.;
                                                         1 EILDV
                                                                                                                                        NASD KLEPN
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                                                                                                                RESULT 10
NASD KLEPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
A Tagami H., Takahashi H., Takeda J., Takemoto K., Uchara K., Wada C.,
A Tagami H., Takahashi H., Takeda J., Takemoto K., Uchara K., Wada C.,
T. Construction of a contiguous 874-kb sequence of the Escherichia coli
T. Construction of a contiguous 874-kb sequence of the Escherichia coli
T. Construction of a contiguous 874-kb sequence of the Innkage map and
analysis of its sequence features.";
T. analysis of its sequence features.";
T. SIMILARITY: BELONGS TO THE HPCH/HPAI ALDOLASE FAMILY.
T. C.I.- SIMILARITY: BELONGS TO THE HPCH/HPAI ALDOLASE FAMILY.
T. C.I.- CAUTION: REP. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE-97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Manu B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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EMBL, D90855; BAA16064.1; -.
EMBL, D90855; BAA16064.1; -.
EMBL, D90855; BAA16068.1; ALT_FRAME.
EMBL, D90856; BAA16068.1; ALT_FRAME.
HSSP, P33522; 1DXE.
ECGENE; EG14083; yfaU.
InterPro; IPR05000; HpcH_HpaI.
Fram: P03338; HpcH_HpaI.
Fram: P03338; HpcH_HpaI.
Hypothetical protein; Lyase; Lyase; Cmplete protecome.
SEQUENCE 267 AA; 28916 MW; F68506D8A11D23FE CRC64;
P76469; P76925; P76928; P76929;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Hypothetical protein yfaU.
YFAU OR B2245.
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PURR LACLA
1D POSSE LACLA STANDARD; F
A 053065;
DT 15-JUN-2002 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
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                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
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222 ÉİLDV 226

RESULT 11 YFAU_ECOLI

1 EILDV 5

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P41010;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                  SPECIES=L.1.lactis; STRAIN=IL1403;
MEDLINE=21235186; PubMed=11337471;
Bolotin R., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
"Tatis sep. lactis IL1403";
Genome Res. 11:731-753(2001).
                                                                                              Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.NCB_TaxID=1360, 1359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Otta S., Yohda M., Ishizuka M., Hirata H., Hamamoto T., Ottawara-Hamamoto Y., Matsuda K., Kagawa Y., Sequence and over-expression of subunits of adenosine triphosphate synthase in thermophilic bacterium PS3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: CONTROLS TRANSCRIPTION OF THE PUR OPERON FOR PURINE BIOSYNTHETIC GENES (By similarity).
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Bacillus PS3 (Thermophilic bacterium PS-3).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase gamma chain precursor (EC 3.6.3.14).
15-JUN-2002 (Rel. 41, Last sequence update) | 15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES=L.1.cremoris; STRAIN=MG1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88163679; PubMed=2894854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ222642; CAA10902.1; -. EMBL; AE006455; AAK06357.1; -.
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                                                           Pur operon repressor.
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Best Local Similarity
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EILDV
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ATPG BACP3
AC P09222
DT 01-MAR
DT 15-JUM
DE ATP 87
GN ATPG 87
CO Bacter
CO Bacter
CO RESULIN
RY SEQUEN
RA OCEASA
RA OCEASA
RA OCEASA
RA CEASA
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P09222
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-!- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
                                                                                                                                                                                                                                                                  CORB - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(1), BETA(1), GAWAM(1), DELTA(1), RPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
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                                                                                                                                                                                                                                          - THE CATALYTIC
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-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATICA ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CP(0) COMPLEX.
FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.
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                                                                                                                                                           CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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TIGRPAMB; TIGR01146; ATPSYN FIGBRUMB; 1.
PROSITE; PS00153; ATPRASE GAMMA; 1.
Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport.
PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN 5 286 ATP SYNTHASE GAMMA CHAIN SEQUENCE 286 AA; 32248 MW; ABB96F687C999252 CRC64.
                                                                                                                                                                                                                                      -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FUN-2002 (Rel. 41, Last annotation update)
ATP synthase gamma chain (EC 3.6.3.14).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR000131; ATPase_gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X07804; CAA30653.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00231; ATP-synt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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les 5, Conserv
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213 EILDV 217
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                                                                   RESULT 16
UBIG RICCN
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                                                                                                            SO THE STATE OF STATE
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removed. Usage by and for commercial ont (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA 31, BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN PAMILY.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                        Length 287;
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100.0%; Pred. No. 1.5e+02; "...matches 0; Indel8
                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 1; Length 28
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; IndelB
                                                                                                        InterPro; IPR000131; ATPase_gamma.
Pfam; PR00231; ATP-Bynt; 1.
PRINTS; PR00126; ATP-Bynt; 1.
TIGRFAMS; TIGR01146; ATPSYN Flgamma; 1.
TIGRFAMS; TIGR01146; ATPSYN Flgamma; 1.
ATP STOTIE; P800153; ATPASE GAMMA; FALSE NEG.
ATP SYNTHesis; CF(1); Hydrogen ion transport; Hydrolase.
SEQUENCE 287 AA; 32343 MW; BA039503BDIFIE5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR000131; ATPase_gamma.
Pfam; PF00231; ATP-synt; 1.
PRINTS; PR00126; ATPASEGAMA.
TIGRPAM; TIGR01146; ATPASE GAMMA; PIGARMA; TIGRO1153; ATPASE GAMMA; FALSE NEG.
ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase.
SEQUENCE 287 AA; 32391 MW; 78A9FB92E01BAE6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus.
Bacteria, Firmicutes, Bacillales, Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase gamma chain (BC 3.6.3.14).
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                    entities requires a license agreement ( or send an email to license@isb-sib.ch)
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and this statement is
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                                                                                     EMBL; D38058; BAA07247.1;
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100...
5. Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                          213 EILDV 217
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P42007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
-!- CATAL/YIC ACTIVITY: S-adenosyl-L-methionine + 3-demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquinone-9.
-!- PATHWAY: Ubiquinone blosynthesis.
-!- PATHWAY: Ubiquinone blosynthesis.
-!- SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
MEDLINE=21442076.
Squta H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64) (3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Symechococcus sp. (strain PCC 7942) (Anacystis nidulans R2)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 1; Length 289, 100.0%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001601; Methyltransf.
Interpro; IPR000051; SAM bind.
TIGREAMS; TIGR01045; PEF; 1.
Ubiquinone blosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPE1 INSERT. 4CAEA6827EC78977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-UTN-2002 (Rel. 41, Last annotation update)
Phytoene synthase (EC 2.5.1.-).
  289 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33074 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
5; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                              metĥyltrânsferase).
                                                                                                                                                                                                                                   Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
DOMAIN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                              NCBI_TaxID=781;
                                                                                                                                                                                                           UBIG OR RC0965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 EILDV 108
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P37269;
UBIG RICCN
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           Complete proteome.
SEQUENCE 320 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                            38 EILDV 42
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P22194;
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                                                                                                                                                                                                                                                                                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 29342 / M129;
MEDLINE=Z108919; PubMed=11271496;
MEDLINE=Z108919; PubMed=11271496;
Herrmann R., Frank R.;
"Towards a two-dimensional proteome map of Mycoplasma pneumoniae.";
Electrophoresis 21:3765-3780(2000).
                                                                                                                                                             CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate
                                                                                                                                                                                                                                        PATHWAY: Carotenoid biosynthesis.
SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY
              CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma pneumoniae.
Bacteria, Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S22200; S22200.
PIR; S22300; S22200.
PIR; S20383; S20383.
InterPro; IPR002060; Squ/phyt_synthse.
PEAM; PR00494; SQQ PSY; 1.
PROSITE; PS01044; SQUALEN_PHYTORN SYN 1; 1.
PROSITE; PS01045; SQUALEN_PHYTORN_SYN 2; 1.
PROSITE; PS01045; SQUALEN_PHYTORN_SYN 2; 1.
SEQUENCE 307 AA; 35781 MW; A13B425F66D10EB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 307; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION BY MASS SPECTROMETRY, AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein MG054 homolog (D09_orf320)
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STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
MEDLINE=92164786; PubMed=1537409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X63873; CAA45350.1; -.
                                                                                                                                                                                 prephytoene diphosphate.
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Best Local Similarity ا00، م
اتم 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                        TO PHYTOENE
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Y054 MYCPN
AC P75049;
DT 01-NOV-1997
DT 01-NOV-1997
DT 15-JUN-2002
DE PETCETA MG054
GN MYCODIAGEN PI
OC SHOOTH PROPERIOR FROM STRAIN-ATCC ARX MEDLINE-97105
RA HIGHMELINE-97105
RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETTMAN RA HETMAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herrmann R.;
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MEDLINE-21948401; PubMed=11859360;
Mod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squores J., Peat N., Hayles J., Basham D., Bowann S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gollins M., Connor R., Cronin A., Davis P., Heltwell T., Fraser A.,
Admiss M., Gonnor R., Themain N., Harris D., Hidagoon G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch B.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Woodward J., Volckaert G., Ast R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Berr P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohkura H., Yanggida M., "8. "8. pombe gene sds22+ essential for a midmitotic transition encodes a leucine-rich repeat protein that positively modulates protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 AA; 36107 MW; ECE3C626C8EAE63F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Procein phosphatases PP1 regulatory subunit sds22.
SDS22 OR SPAC4A8.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 1; L 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 AA
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                                                                                                                                                                                                                                                                                           EMBL, AE000011; AAB95735.1; -.
InterPro, IPR001062; NusG.
Pfam, PP02357; NusG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91098642; PubMed=1846086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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Les 5, Conserv
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[1]
SEQUENCE FROM N.A.
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NCBI_TaxID=60217;
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ID DHAS SHEVI
AC Q56734;
                                                                                                                                                       FAMILY.
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                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-88 (1202).

-I- FUNCTION: ESSENTIAL FOR THE MITOTIC METAPHASE/ANAPHASE TRANSITION. POSITIVETY MODULATES PROTEIN PHOSPHATASE-1. POSSIBLY BY FORMING A PEPRATING HELICAL ROD THAT IS CAPABLE OF ENHANCING A PP1-DEPENDENT DEPHOSPHORYLATIVE AND ACTIVITY.

-I- SUBBUILT: PHYSICALLY INTERACTS WITH THE DISZ AND SDS21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0C7-2001 (Rel. 40, Last annotation update)
Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase)
(ASADH).
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Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                         SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR). SIMILARITY: STRONG, TO YEAST SDS22 AND C.ELEGANS T09AS.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 332; 100.0%; Pred. No. 1.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00560; LRR; 8.
SMART; SM00370; LRR; 10.
SMART; SM00446; LRRcap; 1.
Leucine-rich repeat; Repeat; Mitosis; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF7FBAD984E2A345 CRC64;
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LERR 2.
LERR 3.
LERR 4.
LERR 5.
LERR 6.
LERR 7.
LERR 8.
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EMBL; Z98762; CAB11482.1; -.
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                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear. PTM: PHOSPHORYLATED.
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                                                                                                                                                                                                                                                                                                                                          PIR; A38439; A38439.
HSSP; P09661; 1A9N.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR out.
InterPro; IPR003603; LRRCap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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332 AA;
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Best Local Similarity
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                                                                                                                                                       PHOSPHATASES.
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Q56732;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
SEQUENCE FROM N.A.

MEDLINE=97306055, PubMed=9163523;

Kato C., Smorawinska M., Li L., Horikoshi K.;

Kato C., Smorawinska M., Li L., Horikoshi K.;

"Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenase at elevated hydrostatic pressure in deep-sea bacteria.";

J. Blochem. 121:717-723 (1997).

-[- CATALYTC ACTIVITY: L-aspartate-4-semialdehyde + phosphate +
-[- CATALYTC ACTIVITY: L-aspartyl phosphate + NADPH.

-[- PATHWAY: SECOND STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kato C., Smorawinska M., Li L., Horikoshi K.;

"Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenase at elevated hydrostatic pressure in deep-sea bacteria.";
J. Biochem. 121.717-723 (1997).
-!- CATALYTIC ACTIVITY: L-aspartate-4-semialdehyde + phosphate +
NADP(+) = L-4-asparty1 phosphate + NADPH.
-!- PATHWAY: SECOND STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
TO MET, TO ILE AND TO THR.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase)
                                                                                                                                                                                                                                                                                                                                                                           TO MET, TO ILE AND TO THR.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ASPARTATE-SEMIALDEHYDE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 1; Length 338;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000319; Asp semiald dh.
InterPro; IPR000319; Semialdh dh.
PEam; PF01118; Semialdhyde dh; 1.
PEam; PF02774; Semialdhyde dh; 1.
ITGRFAMS; TIGR01296; asd B; 1.
PROSITE; PS01103; ASD; FĀLSE NEG.
Oxidoreductase; NADP; Diaminopimelate biosynthesis;
Ipysine biosynthesis.
ACT SITE 132 132 BY SIMILARITY.
SEQUENCE 338 AA; 36984 MW; 6BCD8921E4977185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6BCD8921E4977185 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=DSS12;
MEDLINE=97306055; PubMed=9163523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Match
Best Local Similarity 100....
Best Local Similarity 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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modified and this statement is not removed.
                                                                                                                                                               319 3
342 AA;
                                                                                                                                                 Complete proteome.
ACT_SITE 13
ACT_SITE 40
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                199 EILDV 203
                                                                                                                                                                                                                                                                                                                                         1 BILDV 5
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                                                                                                                                                                                                                                                               SEQUENCE
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REPEAT
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REPEAT
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Clostridium perfringens.";
Mol. Gen. Genet. 243:215-224(1994).
-!- CATALYIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell'walls.
-!- SIMILARITY: BELONGS TO FAMILY 25 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canard B., Garnier T., Saint-Joania B., Cole S.T.; "Molecular genetic analysis of the nagH gene encoding a hyaluronidase
                                                                                                                                                                                                                                                                                                                             Gaps
 SIMILARITY: BELONGS TO THE ASPARTATE-SEMIALDEHYDE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H., "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 1; Length 338; 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                         338 AA; 37061 MW; 8D0DC1F46EAF30AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
15-USDable autolytic 1ysozyme (EC 3.2.1.17) (1,4-beta-Nacetylmuramidase) (Autolysin).
                                                                                                                                                                                                            TIGRFAMB; TIGRO1296; asd B; 1.
RNOSITE; PSO1103; ASD; FALSE NEG.
Oxidoreductase; NADP; Diaminopimelate biosynthesis;
Lysine biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                          342 AA.
                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                           InterPro, IPR000319, Asp_semiald_dh.
InterPro, IPR000534; Semialdh_dh.
Pfam; PF01118; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
TIGRFAMS; TIGR01296; asd B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94232189; PubMed=8177218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 256-342 FROM N.A.
                                                                                                                                    EMBL; D49540; BAA08490.1; -. HSSP; P00353; 1BRM.
                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                            132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYC OR CPE0382.
                                                                                                                                                                                                                                                                                                                                                                    BILDV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                flesh-eater."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CPN50;
                                                                                                                                                                                                                                                                                                                                                   1 BILDV 5
                                                                                                                                                                                                                                                                                                                                                                                                                                         LYC CLOPE
P26836;
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                           22
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oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van vuge R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterbock T., Watthey L., McDonald L., Artisch P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn J.J., Butler-Loffredo L., Kieleczawa J., Medalle J., Luft B.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 1; Length 342; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EC3B4078A2FB4732 CRC64;
                                                                                                       EMBL; AP003186; BAB80088.1; -.
EMBL; M81878; AAA23.61.1; -.
InterPro; IPR002053; GH 25.
InterPro; IPR003646; SH3 bac.
Pfam; PF01183; Glyco hydro 25; 1.
SMART; SM00287; SH3, 2.
PROSTIE; PS00953; GLYCOSYL HYDROL F25; 1.
Hydrolase; Glycosidase; Bacteriolytic enzyme; Repeat;
                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
5 X 23 AA TANDEM REPEATS.
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SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last Bequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Flagellar motor switch protein flig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 AA
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-!- SIMILARITY: BELONGS TO THE FLIG FAMILY
                        entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39557 MW;
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Gaps

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Length 351;

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277 GGR -> DVF (IN ISOFORM HSJIA)
351 MISSING (IN ISOFORM HSJIA).
38783 MW; 1FA290C6764665F3 CRC64;
                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 1; L 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0;
                                                                                                                                                                                    Chaperone; Neurone; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=84237568; PubMed=6234204;
                                                                   InterPro; IPR002950; Josephin.
InterPro; IPR003903; UIM.
                                                                                                   Pfam; PF00226; DnaJ; 1.
Pfam; PF02809; UIM; 2.
SMART; SMO0271; DnaJ; 1.
PROSITE; PS00636; DNaJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
                                                  InterPro; IPR001623; DnaJ N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                  Genew; HGNC:5228; DNAJB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                       351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   275
278
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                                 MIM; 604139;
                                                                                                                                                                                                                                                                                                                                                                               1 EILDV 5
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VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DnaJ homolog subfanily B member 2 (Heat shock 40 kDa protein homolog 1) (HSJ-1).
DNAJB2 OR HSJ1 OR HSPF3.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISION TO 214.

Cheetham M.E.;

Submitted (JUL-1998) to the SWISS-PROT data bank.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HSJIA AND HSJIB (SHOWN HERE);
ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: BRAIN (NEURONAL LAYERS). WEAKLY, IN SKELETAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheetham M.E., Brion J.-P., Anderton B.H.;
"Human homologues of the bacterial heat-shock protein DnaJ are
preferentially expressed in neurons.";
Blochem. J. 284:465-476(1992).
                                                                                                                                                                                                                                                                                                                                                                               Length 344;
                                                                                                                                                                                                                                                                                                           Chemotaxis, Flagella, Flagellar rotation, Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 34 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             DF6FDCAADFB3AD8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 AA
                                                                                                                                                                                                                                InterPro; IPR00090; Flg_Motor_Flig. Pfam; PF01706; Flig-C; 1. PRINTS; PR00954; FLGMOTORFLIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 1 J DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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EMBL; X63368; CAA44969.1; ALT SEQ.
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MEDLINE=92287055; PubMed=1599432;
                                                                                                                                                                                                                                                                                                                                             344 AA; 39006 MW;
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HSSP; Q9WY63; 1QC7.
TIGR; BB0290; -.
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SEQUENCE 344 AA
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Obmori H., Kimura M., Nagata T., Sakakibara Y.; "Structural analysis of the dnaA and dnaN genes of Escherichia coli."; Gene 28:159-170(1984).
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MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MAY C.-G., Ohteubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KI2 / MGIG55,
MEDLINE=93315143; PubMed=7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication.";
Genomics 16:551-561(1993).
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MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
11-JUL-1986 (Rel. 01, Created)
01-ARR-1988 (Rel. 07, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DMA Polymerase III, beta chain (EC 2.7.7.7).
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EMBL; M18825. AAA24512.1; --
EMBL; KO2179; AAA24510.1; --
EMBL; XO4341; CAA27869.1; --
PIR; BA2494; DDEC3B.
PIR; AZ2168; A22168.
PDB; 2POL; 31-JAN-94.
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        AE000447; AAC76724.1;
AE005601; AAG58898.1;
AP002566; BAB38059.1;
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SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA DIMENIZATION TO FORM THE POILII' COMPLEX. POLIII' ASSOCIATES WITH THE GAMMA, DELIA, DELIA', PSI, AND CHI) AND WITH THE BETA CHAIN. THE FINAL COMPOSITION OF THE COMPLEX IS: (ALPHA, EPSILON, THETA) [2] - TAU[2] - (GAMMA, DELTA, DELTA', PSI, CHI) [2] - BETA [4]. THE BETA CHAIN IS AN HOMODIMER, WHEN NOT ASSOCIATED WITH THE OTHER COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 342-366 FROM N.A.
MEDLINE-84297235; PubMed-6089112;
Adachi T., Mizuuchi K., Menzel R., Gellert M.;
"DNA sequence and transcription of the region upstream of the E. coli
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MEDLINE=86301872; PubMed=3527871;
Armengod M.E.E., Lambies E.;
"Overlapping arrangement of the recF and dnaN operons of Escherichia coli; positive and negative control sequences.";
Gene 43:183-196(1986).
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MEDLINE-84272685; PubMed-6379647;
MEDLINE-84272685; PubMed-6379647;
MALBARAR M.A., Sandler S.J., Armengod M.-E., Ream L.W., Clark A.J.;
"MOLOCULAR analysis of the reof gene of Bscherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 81:4622-4626(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=92257585; PubMed=1349852;
Kong X.-P., Onrust R., O'Donnell M., Kuriyan J.;
Kong C.-P., Onrust B., O'Donnell M., Kuriyan J.;
"Three-dimensional structure of the beta subunit of E. coli DNA polymerase III holocarzyme: a sliding DNA clamp.";
Cell 69:425-437(1992).
Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterchamorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                           MEDLINE-88298898; PubMed-2841344; Armengod M.E.B., Garcca-Sogo M., Lambies B., Transcriptional organization of the dnaN and recF genes of Escherichia coli K-12."; J. Biol. Chem. 263:12109-12114(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 12:6389-6395(1984).
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SEQUENCE OF 1-14 FROM N.A.
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SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA CHAINS) THAT ASSOCIATES WITH A TAW SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLILI' COMPLEX. POLILI' ASSOCIATES WITH THE GAMMA, DELTA, DELTA, PSI, COMPLEX IS COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI, COMPLEX IS: (ALPHA, EPSILON, THE FINAL COMPOSITION OF THE COMPLEX IS: (ALPHA, EPSILON, THETA) [2] - (GAMMA, DELTA, DELTA', SUBCELLULAR LOCATION: CYtoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
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Skovgaard O., Hansen F.G.;
"Comparison of dnah nucleotide sequences of Escherichia coli,
"Comparison of dnah nucleotide sequences of Escherichia coli,
"Salmonella typhimurium, and Serratia marcescens.";
J. Bacteriol. 169:3976-3991(1987)
-!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT
IS CLAMPED ONTO DNA, IT SLILDE FREELY (BIDIRECTIONAL AND ATP-
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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364 364 364 366 MW; 7A45646F61255B5A CRC64;
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
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-!- FUNCTION: P37 IS PART OF A HIGH-AFFINITY TRANSPORT SYSTEM.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
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CHAIN 27 380 HIGH AFFINITY TRANSPORT SYSTEM PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 1; Length 366; 100.0%; Pred. No. 1.98+02; ive 0; Mismatches 0; Indels
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380 AA; 43495 MW; BREBDE2199CCC792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                     SMART, SN00480, POLJBC, 1.
TIGRFAMs; TIGR00663; dnan; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                 366 AA, 40548 MW, 575FD8F13D928742 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P37 MYCPN STANDARD; PRT; 380 AA.
P75371;
01-NOV-1997 (Rel. 35, Created)
11-NOV-1997 (Rel. 35, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
11910 affinity transport system protein P37 precursor.
P37 OR MPM415 OR MP425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AE000041; AAB96073.1; -- PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
EMBL, AF034747; AAB87631.1; -.
EMBL, AE008899; AAL22696.1; -.
EMBL, MI7352; AAA02816.1; -.
HSSP; P00583; ZPOL.
Stydene; SG10089; dnaN.
InterPror; IPRO01001; DNA pollII beta.
Pfam; PF00712; DNA pol3 beta 1.
Pfam; PF02767; DNA pol3 beta 2; 1.
Pfam; PF02767; DNA pol3 beta 3; 1.
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SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
1es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumoniae."
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Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
      Hypothetical protein yxeP
                                                                                                                          NCBI TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

C STRAIN=VCI 16 / DSM 4304 / ATCC 49558;

KARANI=VCI 16 / DSM 4304 / ATCC 49558;

KIGHK H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

A Kienk H.-P., Clayton R.J., Gwinn M., Hickey B.K., Peterson J.D.,

A Kienkardson D.L., Kerlavage A.R., Grahm D.E., Kyrpides N.C.,

A Richardson D.L., Verlavage A.R., Grahm D.E., Kyrpides N.C.,

A Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McMenil J.K., Badger J.H., Glodek A., Zhou L.,

A Overbeek R., Gacayne J.D., Weidman J.F., McDonald L., Utterback T.,

Sadow P.W., D'Andres K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2010 (Rel. 40, Last annotation update)
RDNA-directed RNA polymerase subunit A" (EC 2.7.7.6).
RPOA2 OR API889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                              380 AA
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                                                                                                                                                           PRT;
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                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                  Archaeoglobus fulgidus.
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Hes 5; Conserv
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   370 EILDV 374
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01-OCT-1996
15-JUN-2002
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YXEP_BACSU
ID _YXEP_BACSU
AC P54955;
                                                                                                                          RPA2_ARCFU
ID RPA2_ARCFU
AC 028390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAK KUNBLIALES DAYANGERE I, Albertini A.M., Alloni G.,
RA KUNBE F., Oggaswara N., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Brunscher L., Brans A., Braun M., Briggiell S.C., Bron S.,
RA Brouillet S., Brunschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizor F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sarlan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sarlor F.,
Schleich S., Schroceter R., Scoffone F.,
Sckowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sacorin M., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Taragi T., Takabashi H., Takemaru K.,
RA Takadul M., Wandulet R., Wedler R., Vasumoto K., Yasumoto K., Pohlice Gram-positive bacterium Bacillus
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                                STRAIN=168 / BGSC1A1;
MEDLINE=97021444; PubMed=8867804;
WEDLINE=97021444; PubMed=88, Yanai N., Fujita Y.;
"Cloning and sequencing of a 23-kb region of the Bacillus subtilis genome between the iol and hut operons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subtitist, BG11892, yxep.

InterPro; IPR003933; Peptidase M20.

InterPro; IPR01933; Peptidase M20.

InterPro; Pr01546; Peptidase M20, Interpro; Pr01546; Peptidase M20, Interpro; Pr01546; Peptidase; Complete proteome.

SEQUENCE 380 AA; 41596 MW; BD149964FAE42118 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:249-256(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M40.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D45912; BAA08332.1; -. EMBL; Z99124; CAB15983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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les 5; Conserv
                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A
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277 EILDV 281

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44 EILDV

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RESULT 31
CEGT HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS INTRODUCED FROM POSITION 112-135 TO EXTEND THE SIMILARITY WITH THE
                                                                                                                                                                                                                                                                                                                                                                                            UDDDDISHED OBSERVATIONS (JAN-2000).

-I- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND FALSO MIGHT DIRECT THE SELECTIVITY AND FALSO MIGHT DIRECT THE COMPARTMENT. INTERACTS WITH CYCLING (IN VITRO).

-I- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 16 KDD ACOMONITY (CONSTANT REGULATORY SUBUNIT (PREDUIT A), THAT ASSOCIATE WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS.

B (THE R2/B)FRESS/BS5, R3/B'', /PR72/PR130/PRS9 AND R5/B'/BS6
FAMILIES), THE 48 KDB VARIABLE REGULATORY SUBUNIT; VIRAL PROTEINS, AND CELL SIGNALING MOLECULES.
                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sanctation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, epsilon isoform (PSZA, B subunit, B epsilon isoform) (PPZA, B subunit, B subunit, B56 epsilon isoform) (PPZA, B subunit, RF epsilon isoform) (PPZA, B subunit, RF epsilon isoform) (PPZA, B subunit, RF epsilon isoform) (Pragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                            'p53-dependent association between cyclin G and the B' subunit of
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUB=Embryonic fibroblast;
MEDLINE=97042488; PubMed=8887688;
Okamoto K., Kamibayashi C., Serrano M., Prives C., Mumby M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 1; Length 387; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 AA; 45497 MW; 780D5404848A548E CRC64;
            387 AA
                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION OF PROBABLE FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U49728; AAB37234.1; ALT_FRAME.
MGD; MGI:1349473; PPD2156.
ILITEMPRO, IPRO02554; B56.
Pfam; PF01603; B56; 1.
                                                                                                                                                                                                                                                                                                                       protein phosphatase 2A.";
Mol. Cell. Biol. 16:6593-6602(1996).
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN HOMOLOG.
                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family.
          ZASE MOUSE
Q61151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                Beach D.;
                                                                                                                                                                                                                                                                                                                                                                                     Hulo C.;
                                                                                                                                              PPP2R5E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 93:4638-4643(1996).
-!- FUNCTION: MAY SERVE AS "FLIPPASE" AS WELL AS A GLUCOSYLTRANSFERASE
THAT TRANSFERS GLUCOSE TO CERAMIDE.
                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ceramide glucosyltransferase (EC 2.4.1.80) (Glucosylceramide synthase)
(GCS) (UDP-glucose:N-acylsphingosine D-glucosyltransferase) (GLCT-1).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=95209704; PubMed=8643456;
IChikawa S., Sakiyama H., Suzuki G., Hidari K.I.-P., Hirabayashi Y.;
"Expression clonning of a cDNA for human ceramide glucosyltransferase that catalyzes the first glycosylation step of glycosphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucosyl-N-acylephingosine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: UDP-glucose + N-acylsphingosine = UDP + D-
                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001173; Glycos transf 2.
Pfam; PF00535; Glycos transf 2; 1.
Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3B998569F8A96449 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LUMENAL (POTENTIAL).
SIGNAL-ANCHOR (POTENTIAL)
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; Pred. No. 2.1e+02;
0; Mismatches 0;
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  394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D50840; BAA09451.1; -. Genew; HGNC:12524; UGCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
STANDARD;
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DOMAIN
                                                                                                                                                                                                              Homo sapiens (Human)
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394 AA;
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 EILDV 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis.";
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  CEGT HUMAN
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ID YAFA E
AC P04335
DT 20-MAR
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DT 15-JUN
DE Hypoth
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2ASG MOUSE STANDARD; PRT; 415 AA.

060996; 035708;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
8erine/fureonine protein phosphateas 2A, 56 kba regulatory subunit,
8erine/fureonine protein phosphateas 2A, 56 kba regulatory subunit,
B56 gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit,
B56 gamma isoform) (PP2A, B subunit, B' samma isoform) (PP2A, B subunit, B' samma isoform) (PP2A, B subunit, B' samma isoform)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bryant D.W., Rossetto F.E., O'Reilly C., Nieboer E., Turnbull J.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                               Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95004589; PubMed=7920643;
Robison K., Gilbert W., Church G.M.;
"Large scale bacterial gene discovery by similarity search.";
Nat. Genet. 7:205-214(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X63336; -; NOT ANNOTATED_CDS.
StyGene, SG10415; YafA.
InterPro; IPR001039; Ser_estrs_site.
Hypothetical protein; Complete proteome.
20NFLICT 28 30 MG -> CI (IN REF. 2).
SCONFLICT 35 36 MQ -> CI (IN REF. 2).
SEQUENCE 414 AA; 47159 MW; B0B2843A26B263D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 1; L
100.0%; Pred. No. 2.2e+02;
Live 0; Mismatches 0;
                                 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Hypothetical protein yafA.
YAFA OR STM0318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE008709; AAL19274.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-36 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 EILDV 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-LT2:
                                                                                                                                                                                                                                                                  Salmonella.
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1D 2ASG W

AC 060976.

DT 30-MAY.

DT 30-MAY.

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DE Serine,

DE Seri
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      요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAINS-KI2 / W3110;
STRAINS-KI2 / W3110;
Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,
Yamamoto Y., Inokuchi H., Miki T., Hateda E., Fukuda R., Ichihara S.,
Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;
"Systematic sequencing of the Escherichia coli genome: analysis of the
"Systematic sequencing of the Escherichia coli genome: analysis of the
4.0 - 6.0 min (189,987 - 281,416Dp) region.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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NPDKJAGITHOWIEKKEL -> KILTKVFRKSPTGSKNACV
KNLINFANLVKQLHHNRR (IN REF. 1 AND 3).
2CLS4E46CPC9565E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12 / MGI655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                      MEDLINE-88155481; PubMed=6397401;
Nuesch J., Schumperli D.;
Structural and functional organization of the gpt gene region of
Escherichia coli.";
Gene 32:243-249(1984).
YAFA OR B0239.
Bscherichia coli.
Bacteria: Proteobacteria; gamma subdivision, Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis R.W.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 1 AND 3).
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PIR; A04451; QQEC49.
EcoGene; EG11001; yafA.
InterPro; IPR000379; Ser estre site.
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Best Local Similarity 100...
Fra 5; Conservative
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                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                            NCBI_TaxID=562;
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ID YAFA SALTY
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Length 414; 0; Indels

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I-SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS B (THE R2/F)F/R5/F85, R3/F, '/PR72/PR130/PR59 AND R5/B'/B56 FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS, AND CELL SIGNALING MOLECULES.
-I-SUBCELLULAR LOCATION: CYCOPIACM:
-I-PTM: PHOSPHORYLATED ON SERIOR RESIDUES.
-I-SUMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                               Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I., Merlevede W., Goris J., Hemmings B.A.; "The variable subunit associated with protein phosphatase 2A0 defines a novel multimember family of regulatory subunits."; Biochem. J. 317:187-194(1996).
                        Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, epsilon isoform (PP2A, B subunit, B' epsilon isoform) (PP2A, B subunit, B56 epsilon isoform) (PP2A, B subunit, R66 epsilon isoform) (PP2A, B subunit, R76 epsilon isoform).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=96355607; PubMed=8703017; MCCright B., Rivers A.M., Audlin S., Virshup D.M.; Trivers A.M., Audlin S., Virshup D.M.; "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    both nucleus and cytoplasm.";
J. Biol. Chem. 271:22081-22089(1996).
-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 23; DB 1; Length 467; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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Pfam; PF01603; BS6; 1.
Phosphorylation; Multigene family.
SEQUENCE 467 AA; 54699 MW; DD9CE11433F499CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 AA
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 449-455
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                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal retina;
MEDLINE=96276417; PubMed=8694763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z69029; CAA93153.1; -. EMBL; L76703; AAB69752.1; -. Genew; HGNC:9313; PPP2R5E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Fetal brain;
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YAP1_MOUSE
ID _YAP1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentially expressed during melanoma progression.";

differentially expressed during melanoma progression.";

cancer Res. 56:385-3886 (1996).

cancer Res. 56:385-3886 (1996).

clocalization or THE CATIVITY, AND ALSO MIGHT DIRECT THE SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE COMPARTMENT. INTERACTS WITH CYCLIN G IN VITRO.

comparation. INTERACTS WITH CYCLIN G IN VITRO.

composed of 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa CONSTANT REGULATORY SUBUNITS. PROTEINT CONSTANT REGULATORY SUBUNITS. PROTEINT CAND A 65 kDa CONSTANT REGULATORY SUBUNITS. PROTEINT TAT ASSOCIATES WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS.

c I'TH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS.

d I'TH THE R2/8/PRS5/BS5, R3/8''/PR72/PR130/PRS9 AND R5/8'/BS6

FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS, CONNOCCULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND CELL SIGNALING MOLECULES.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
TISSUE SPECIFICITY: HIGHEST LEVELS IN HEART, LIVER AND BRAIN. LOWER
LEVELS IN SKELETAL MUSCLE, SPLEEN, KIDNEY, AND LUNG.
SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                  Tehrani M.A., Mumby M.C., Kamibayashi C., I "Identification of a novel protein phosphatase 2A regulatory subunit highly expressed in muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1708 _TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6;
MEDLINE=96354596; PubMed=8752144;
Francia G., Mitchell S.D., Moss S.E., Hanby A.M., Marshall J.F.,
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; E3C2DF4C57F729C2 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                 Biol. Chem. 271:5164-5170(1996).
                                                                                                                                                                                                            MEDLINE=96214950; PubMed=8617797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 AA; 51196 MW;
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 15-435 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1349475; Ppp2r5c.
InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
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Best Local Similarity
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16-OCT-2001
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SEQUENCE
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                                                                                                                                                                                                                                             STRAIM=NIH Swiss: TISSUE=Embryo;
MEDLINE=95301570; PubMed=7782338;
Sudol M., Bork P., Einbond A., Kastury K., Druck T., Negrini M.,
Huebner K., Lehman D.;
"Characterization of the mammalian YAP (Yes-associated protein) gene
and its role in defining a novel protein module, the WW domain.";
J. Biol. Chem. 270:1473-14741(1995).
-I- FUNCTION: BINDS TO THE SH3 DOMAIN OF THE YES KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=92107187; PubMed=1530878;
Williams L.J., Barnett G.R., Ristow J.L., Pitkin J., Perriere M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 1; Length 472; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
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01-AUG-1992 (Rel. 23, Last sequence update)
01-ULL-1998 (Rel. 36, Last annotation update)
Ornithine decarboxylase (EC 4.1.1.17) (ODC).
                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 AA
               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence upo
15-UUN-2002 (Rel. 41, Last annotation u
65 kDa Yes-associated protein (YAP65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW 1.
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SMART; SM00456; WW; 2.
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DOMAIN 156 189
DOMAIN 215 248
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                                                                                                      YAP1 OR YAP65 OR YAP
                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 472 AA;
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY
Davis R.H.;

"Ornithine decarboxylase gene of Neurospora crassa: isolation,
"Ornithine decarboxylase gene of Neurospora crassa: isolation,
sequence, and polyamine-mediated regulation of its mRNA.";
MOI. Cell. Biol. 12:347-359(1992).
-!- CATALYTIC ACTIVITY: L-ornithine = putrescine + CO(2).
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- ENZYME REGULATION. ODC SYNTHESIS IS ENHANCED POSTRANSCRIPTIONALLY
BY AN EXCESS OF PUTRESCINE. THIS POLYAMINE-MEDIATED CONTROL IS
UNIQUE TO N.CRASSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR
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"Identification of a new family of protein phosphatase 2A regulatory
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...., Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; Q15712; 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Q15712; Q15712; Q15
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PROSITE; PS00878; ODR DC 2 1; 1.
PROSITE; PS00879; ODR DC 2 2; 1.
Lyame; Decarboxylame; Pyridoxyl phosphare; Polyamine biosynthesis.
BINDING 114 114 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; M68970; AAA33605.1; -.
EMBL; L16920; AAA33614.1; -.
PIR; A42065; A42065.
HSSP; P07805; 1P3T.
InterPro; IPR000183; Decarbxy18e2.
Pfam; PP00278; Oxn DAP Arg dec; 1.
Pfam; PF02784; Oxn DAP Arg dec; 1.
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J. Biol. Chem. 270:26123-26128(1995)
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Matches 5; Conservative
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(OPRtase); Orotidine 5'-phosphate decarboxylase (EC 4:1.1.23)
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47
493 AA;
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                                                                                                 NCBI_TaxID=7227;
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ID 2A5B_HI
AC Q15173;
DT 30-MAY-
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                                    Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I., Merlevede W., Goris J., Hemmings B.A.;
"The variable subunit associated with protein phosphatase 2A0 defines a novel multimember family of regulatory subunits.";
Biochem. J. 317:187-194(1996).
                                                                                                                                                                                                                                                                             SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa CONTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES WITH A VARLETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATES WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS BY THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNITS, AND CELL SIGNALING MOLECULES.
                                                                                                                                                                                           both nucleus and cytoplasm.";
J. Biol. Chem. 271:22081-22089(1996).
-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                     MEDLINE-96355607; PubMed-8703017;
McCright B., Rivers A.M., Audlin S., Virshup D.M.;
"The B56 family of protein phosphatase 2A (PP2A) regulatory subunits
encodes differentiation-induced phosphoproteins that target PP2A to
                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY; WIDELY EXPRESSED WITH THE HIGHEST EXPRESSION
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Q01637; Q24221;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Uridine 5'-monophosphate synthase (UMP synthase) (Rudimentary-like protein) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10)
                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: PHOSPHORYLATED ON SERINE RESIDUES.
SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
PAMILY.
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H -> S (IN REF. 2; AA SEQUENCE)
R -> E (IN REF. 2; AA SEQUENCE)
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SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D31407F7032A6D44 CRC64;
                                                                                                                           PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
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Pfam; PF01603; B56; 1.
Phosphorylation; Multigene family.
                           MEDLINE=96276417; PubMed=8694763;
                                                                                                                                                                                                                                                                                                                                                                                                                        IN HEART AND SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 52 E
54 54 H
451 451 R
486 AA; 56193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L42373; AAC37601.1; -. Genew; HGNC:9309; PPP2R5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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54
451
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 601643;
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                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota; Metezoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                 MEDLINE-91042409; PubMed-2122228;
Eisenberg M.T., Gathy K., Vincent T., Rawls J.;
"Molecular cloning of the UMP synthase gene rudimentary-like from
Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRPAMS; TIGRO0336; PYTE; 1.
PROSITE; PS00103; PUR PYR PR TRANSFER; 1.
PROSITE; PS001164; OMPDECASE; Multifunctional enzyme; Transferase; Glycosyltransferase; Lyase; Decarboxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 1; Length 493; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                            SEQUENCE FROM N.A.
Eisenberg M.T., Kirkpatrick R., Rawls J.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REF. 2)
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGLPQ -> YPDVM (IN
56479CDAB1F6A308
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OMPDECASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro, IPR001754; OMPdecase.
Interpro, IPR00836; PRTransferase.
Interpro, IPR002375; Pr/py_rp_transf.
Interpro, IPR04467; PyrE.
Pfam; PF00156; Pribosyltran; 1.
Pfam; PF00155; OMPdecase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Q15173; Q13853;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53327 MW;
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EMBL; X54230; CAA38138.1; -.
PIK; S11907, S11907.
HSSP; P03962; LDQW.
Flybase; FBGN0003257; r-l.
                                                                                                                                                                                                                                                                      SEQUENCE OF 1-78 FROM N.A.
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493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!-SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA COMPOSED OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA CONEDARY REGULATORY SUBUNIT (SUBUNIT ASSOCIATES WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56 FAMILIES), THE 48 KDA DANIALES OF REGULATORY SUBUNIT, VIRAL PROTEINS, AND CELL SIGNALING MOLECULES.
-!- SUBCELLULAR LOCATION: CYCOPIASMIC.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-1 (SHOWN HERE) AND BETA-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN.
-!- THAN AT LEAST ISOFORM BETA-1 IS PHOSPHORYLATED ON SERINE RESIDUES.
-!- PTM: AT LEAST ISOFORM BETA-1 IS PHOSPHARSE, 2A REGULATORY SUBUNIT B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=96276417; PubMed=8694763;
Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I.,
Merlevede W., Goris J., Hemmings B.A.;
"The variable subunit associated with protein phosphatase 2A0 defines
a novel multimember family of regulatory subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           both nucleus and cytoplasm.",
J. Biol. Chem. 271:22081-22089(1996)
-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
Phosphorylation; Alternative splicing; Multigene family.
VARSPLIC 1 19 METKLPPASTPTSPSSPGL -> MITVNPPLPQDTVNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
MEDLINE=56355607: PubMed=8703017;
MCCright B., Rivera A.M., Audlin S., Virshup D.M.;
"The B56 family of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to
                                                                                                                                                                                                                                                                                                                         MEDIINE=96064678; PubMed=7592815;
McCright B., Virshup D.M.;
"Identification of a new family of protein phosphatase 2A regulatory
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Setine/threonine protein phosphatase 2A, 56 KDa regulatory subunit,
beta isoform (PP2A, B subunit, B' beta isoform) (PP2A, B subunit,
B56 beta isoform) (PP2A, B subunit, PR61 beta isoform) (PP2A, B subunit,
subunit, R5 beta isoform).
                                                                                                                                                                                         Vertebrata; Euteleostomi;
                                                                                                                                                                                    Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM BETA-2), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 270:26123-26128(1995).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM BETA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 142374; AAC37602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z69028; CAA93152.1; -. HGNC:9310; PPP2R5B.
                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                          rissum=Fetal brain;
                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPARTMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601644;
                                                                                                                                                                                                                                                                                                                                                                                                      subunits."
                                                                                                                                              PPP2R5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
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                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96161994; PubMed=8576224;
Csortos C., Zolnierowicz S., Bako B., Durbin S.D., Depaoli-Roach A.A.;
"High complexity in the expression of the B' subunit of protein
phosphatase 2Ao. Evidence for the existence of at least seven novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (5) AND A 65 kDa
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (5) THAT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
B (THE R2/B/PR55/B55, R3/B*, /PR72/PR130/PR59 AND R5/B*/B56
FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: HIGHER REPRESSED IN BRAIN.
-!- SILLARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoforms.";
J. Biol. Chem. 271:2578-2588(1996).
J. Biol. Chem. 271:2578-2588(1996).
-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
Berine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
Beta isoform (PP2A, B subunit, B' beta isoform) (PP2A, B subunit,
B56 beta isoform) (PP2A, B subunit, PR61 beta isoform) (PP2A, B
subunit, R5 beta isoform) (PP2A, B subunit, B'-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotay Caminarian (marata)
Bukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: NOMENCLATURE USED IN REP.1 REFERS TO PP2A B SUBUNIT BY ALPHA ISOFORM, WHICH IS CITED AS PP2A B SUBUNIT BETA-PR61 ISOFORM IN LATER PUBLICATIONS.
(IN ISOFORM BETA-2).
QB -> IF (IN REF. 2; AA SEQUENCE).
ES -> GA (IN REF. 2; AA SEQUENCE).
F -> M (IN REF. 2; AA SEQUENCE).
S -> M (IN REF. 2; AA SEQUENCE).
W -> E (IN REF. 2; AA SEQUENCE).
W -> E (IN REF. 2; AA SEQUENCE).
                                                                                                                                                                                          ö
                                                                                                                                                    Length 497;
                                                                                                                                     Score 23; DB 1; Length 4>
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                   500 AA
                                                                                                                                                                                            0, Mismatches
                   58 QE
178 ES
181 F
184 S
461 W
57393 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit)
                                                                                                                                                    100.0%;
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                     57
177
181
184
461
497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=New Zealand;
                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                           2A5B RABIT
028647;
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                   CONFLICT
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EMBL, U37769, AAC48527.1; -. InterPro, IPR002554; B56. Pfam; PF01603; B56; 1.

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999)
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate + glycyl-tRNA(Gly).
-!- GUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGR00389; GlyS dimeric; 1.
PROSITE; PSS0862; AA TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; ProteIn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                    STRAIN=R1;
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
GLYS OR DR2059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                         Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 1; Length 506; llarity 100.0%; Pred. No. 2.7e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  506 AA; 57204 MW; 23A7C69DE83D2D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FINC_CANFA STANDARD; PRT; 522 AA. Q28275; Q28275; Q28276; Q28276; Q28070-1997 (Rel. 35, Created) 16.00V-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Fibronectin (FN) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001106; AAtRNA_ligaseII.
InterPro; IPR004154; HGPP anticodon.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002315; tRNA-synt_gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002042; AAF11606.1; ALT_INIT.
HSSP; P56206; 1ATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00587; tRNA-synt 2b; 1.
Pfam; PF03129; HGTP anticodon; 1.
PRINTS; PR01043; TRNASYNTHGLY.
                                                                                                                                                        Deinococcaceae; Deinococcus.
                                                                                                 Deinococcus radiodurans.
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Matches 5; Conserv
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE 506 AA;
                                                                                                                                                                                     NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; DR2059; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 EILDV 280
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FINC_CANFA
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                                                                                                                                 Gaps
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-!- PATHWAY: Glycerol utilization; rate-limiting step.
-!- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE / GLYCEROKINASE / XYLULOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-DUN-20002 (Rel. 41, Last annotation update)
Glycerol Kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
(Glycerokinase) (GK)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas tolaasii.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                            Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 503; 100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; Length 50
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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Multigene family; Nuclear protein.
SEQUENCE 500 AA; 57709 MW; 001CA9360E4C04B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                503 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murata H.;
"GlpK of Pseudomonas tolaasii.";
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ID SYG_DEIRA STANDARD;
AC QPSER5;
DT 16-OCT-2001 (Rel. 40, Created)
                                                                                                 Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=29442;
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Gaps

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Matches

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RA MEDIANE=96324983; PubMed=8702559;

RA MACLEOD JAN., Burton-Wurter N., Gu D.N., Lust G.;

Racleod J.N., Burton-Wurter N., Gu D.N., Lust G.;

RI "Fibronectin mRNA splice variant in articular cartilage lacks bases

RT "Fibronectin mRNA splice variant in articular cartilage lacks bases

RT "Fibronectin mRNA splice variant in articular cartilage lacks bases

RT "Fibronectin mRNA splice variant in articular cartilage lacks bases

RT "Fibronectin mRNA splice variant in Seqments.";

L. Biol. Chem. 271:18954-18960(1996).

C. I- FUNCTION: PIBRIN, HEBRAIN, DNA, AND ACTIN. FIBRONECTINS

C. I- FUNCTION: VARIANT (V+C)- IS PROBABLY INVOLVED IN MATRIX

C. I- FUNCTION: VARIANT (V+C)- IS PROBABLY INVOLVED IN MATRIX

C. I- FUNCTION: VARIANT (V+C)- IS PROBABLY INVOLVED IN MATRIX

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C. I- FUNCTION: VARIANT (V+C)- IS PROBABLY INVOLVED IN MATRIX

C. I- FUNCTION: VARIANT IN SOME FORMS OF FIBRONECTING STRAND3;

C. I- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING STRAND3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN OTHERS. THESE DIFFERENCES ARE DUE TO A LISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMRRIC FORM) IS SECRETED BY HERDAUCTINES. THE CALLILAR FN (SOLUBLE DIMRRIC FORM)

BY HERPATOCYTES. CELLULAR FN (SOLUBLE DIMRRIC FORM) IS SECRETED BY HERPATOCYTES. CELLULAR MATRIX. VARIANT (V+C)- IS THE MAJOR TRANSCRIPT IN ARTICULAR CARTILAGE, BUT IT IS ABSENT FROM LUYER.

C. I- FUNCTION WALLEY FOR TRANSCRIPT IN ARTICULAR CARTILAGE, BUT IT IS ABSENT FROM LUYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEPARIN-BINDING 2 (BY SIMILARITY).
FIBRIN-BINDING 2 (BY SIMILARITY).
FIBRONECTIN TYPE-111 14.
FIBRONECTIN TYPE-111 15.
CONNECTING STRAND 3 (CS-3) (V REGION).
FIBRONECTIN TYPE-111 16.
FIBRONECTIN TYPE-11 10.
FIBRONECTIN TYPE-1 10.
FIBRONECTIN TYPE-1 11.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SULFATION (POTENTIAL).
N'LINKED (GLCNAC. . .) (POTENTIAL).
D -> E (IN ISOFORM (V+C)-).
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EMBL, US2106; AAC48611.1; --
HSSP; POZ751; IFNH.
INTERPRO; IPR003961; FN III.
INTERPRO; IPR00083; Fibrnctn1.
Pfan; PF00041; fn1; 3.
Pfan; PF00041; fn1; 3.
SMART; SM00069; FN1; 2.
SMART; SM00069; FN3; 3.
Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion; Nonestic Sulfation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: SULFATED (BY SIMILARITY).
SIMILARITY: CONTAINS AT LEAST 4 PIBRONECTIN TYPE III DOMAINS.
SIMILARITY: CONTAINS AT LEAST 3 FIBRONECTIN TYPE I DOMAINS.
                           SEQUENCE FROM N.A., AND VARIANT (V+C)-.
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                                                                                                                                                                                                                                      Gapa
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Eguus.
                                                                                                                                                                                                                                      ö
                                                                                                                                                          Length 522;
   MISSING (IN ISOFORM (V+C)-).
                                                                                                                                                                                                                                      0; Indels
                                                                               57700 MW; DB1D9A54C2BDAE26 CRC64;
                                                                                                                                                      Score 23; DB 1; I
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Fibronectin (FN) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       522 AA
                                                                                                                                                                                                                                      0; Mismatches
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InterPro; IPR000083; Fibrnctn1
                                                                                                                                                          100.0%;
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                                                                                                               Query Match

Best Local Similarity 100.v.

5; Conservative
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206 4
522 5
522 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FINC HORSE (Q28378;
                                                                                                                                                                                                                                                                                                                                                                                        222 EILDV 226
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VARSPLIC
NON TER
SEQUENCE
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Query Match
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                                                                                           FIBRUN-BINDING 2 (BY SINILARITY).
FIBRONECTIN TYPE-III 13.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 15.
CONNECTING STRAND 3 (CS-3) (V REGION).
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 10.
FIBRONECTIN TYPE-I 11.
FIBRONECTIN TYPE-I 11.
FIBRONECTIN TYPE-I 11.
FIBRONECTIN TYPE-I 12.
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
D-> E (IN ISOFORM (V+C)-).
MISSING (IN ISOFORM (V+C)-).
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tehrani M.A., Mumby M.C., Kamibayashi C.;
"Identification of a novel protein phosphatase 2A regulatory subunit highly expressed in muscle", "highly expressed in muscle", "biol. Chem. 271:5164-5170(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                           2ASG HUMAN STANDARD; PRT; 524 AA.

Q13362; Q14391; Q15174; Q1506;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit, R'S gamma isoform).
Pfam; PF00039; fn1; 3.
Pfam; PF00041; fn3; 3.
SMART; SM0058; FN1; 2.
SMART; SW00060; FN3; 3.
PROSITE; PS01253; FIBRONECTIN 1; 2.
Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                     HEPARIN-BINDING 2 (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                  0; Indels
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100.0%; Pred. No. 2.8e+02;
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                                                             Repeat; Sulfation; Alternative splicing.

NON TER 1 204 HEPARIN-BIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM GAMMA-3).
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MEDLINE=96214950; PubMed=8617797;
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522 AA;
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Best Local Similarity
Matches 5; Conserv
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YTVYSQASTWSIPVAMETDGPLFEDVQMLRKTVKDEAHQAQ
KDPKKDRPLALRKSELPQDPHTKKALBAHCRADELASQDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96355607; PubMed=8703017;
MGCTight B., Rivers A.M., Audlin S., Virshup D.M.;
"The B56 family of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to
                                                                                                                                                                                                                                                                  SEQUENCE OF 11-524 FROM N.A. (ISOFORM GAMMA-1).
MEDLINE=96064678; PubMed='592815;
MECTIGHT B., Virsh PubMed=''
"Identification of a new family of protein phosphatase 2A regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
TISSUE=Bone marrow;

MEDILE=$6051399, PubMed=7584044;

MEDILETE=$6051399, PubMed=7584044;

Seki N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,

Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;

"Prediction of the coding sequences of unidentified human genes. II.

The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by

analysis of cDNA clones from human cell line KG-I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           both nucleus and cytoplasm.";
J. Biol. Chem. 271:22081-22089(1996).
-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- VLKKRIT (IN ISÖFORM GAMMA-1).
MISSING (IN ISOFORM GAMMA-2).
L -> R (IN REF. 3).
28EBF54550710C19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
Nuclear protein; Phosphorylation; Alternative splicing; Multigene family.
DOMAIN 416 422 NUCLEAR LOCALIZATION SIGNAL VARSPLIC 443 524 VTUVCARCARCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 270:26123-26128(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U37352; AAC50387.1; ALT_INIT.
EMBL; Z69030; CAA93154.1; -
EMBL, D26445; BAA05465.1; -
EMBL, L42375; AAC37603.1; -
Genew; HGNC:9311; PPP2R5C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61017 MW;
                                                                                                                                                                                                           DNA Res. 1:223-229(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 4
494 4
524 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             subunits."
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CONFLICT
SEQUENCE
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Length 524;

DB 1;

Score 23;

100.00;

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DOMAIN

A72 489 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
VARSPLIC 482 524 AQKDPKKERPLARRKSELPQDPHTKKALEAHCRADELVPQD
GR -> QLVGRKAVSSTQVRKV (IN ISOFORM GAMMA-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=New Zealand; TISSUE=Skeletal muscle;
MEDLINE=96161994; PubMed=8576224;
CSOTTOS C., Zolnierowicz S., Bako E., Durbin S.D., Depaoli-Roach A.A.;
"High complexity in the expression of the B' subunit of protein phosphatase 2A0. Evidence for the existence of at least seven novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS: 4 ISOFORMS; GAMMA-1/BETA-4, GAMMA-3/BETA-
3 (SHOWN HERE), GAMMA-4/BETA-1 AND GAMMA-5/BETA-2; ARE PRODUCED BY
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES WITH A VARLETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE WITH THE CORE DIMER INCLUDE THREE PAMILIES OF REGULATORY SUBUNITS BY THE CORE DIMER INCLUDE THREE PAMILIES OF REGULATORY SUBUNITS PAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNITS AND CELL SIGNALING MOLECULES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Niol. Chem. 271:2578-2588(1996).
FUNCTION: THE B REGULATORY SUBDITY, AND ALSO MIGHT DIRECT THE SELECTIVITY AND CAPALYTIC SCTIVITY, AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                       Q28651; Q28648; Q28650; Q28652; Q28651; Q28648; Q28651; Q28648; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650; Q28650
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                     0; Indels
Pred. No. 2.8e+02;
Mismatches 0;
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EMBL; U37770; AAC48528.1; -.
EMBL; U38190; AAC48529.1; -.
      100.08;
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                                     Conservative
   Best Local Similarity
Matches 5; Conserv
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AQKOPKKERPLARRKSELPQDPHTKKALEAHCRADELVPQD
GR -> VKVPG (IN ISOPORM GAMMA-5)
YSLCSHASTVSMPLAMETDGPLEBDVQMLRKTVSDEARQAQ
YSPKKERPLARRKSELPQDPHTKKALEAHCRADELVPQDGR
-> VLKKRAI (IN ISOPORM GAMMA-1)
DC4520D122DAF386 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                      Gaps
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-!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
diphosphate + L-methionyl-tRNA(Met).
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- SUBJUIT: HOWODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kibhi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
-!- FUNCTION: IT IS PROBABLY ESSENTIAL FOR CELL SURVIVAL, BEING REGUIRED NOT ONLY FOR ELLOWITION OF PROTEIN SYNTHESIS BUT ALSO FOR THE INITIATION OF ALL MENA TRANSLATION THROUGH INITIATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYM CHLPN STANDARD; PRT; 551 AA.
09255; Q9JRW1;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
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                                                                                                                                                                                                                                       Length 524;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
NCBI_TaxID=83558;
                                                                                                                                                                                                                                    100.0%; Score 23; DB 1; L. larity 100.0%; Pred. No. 2.8e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRONG, TO CYSTEINYL-TRNA SYNTHETASE.
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Nucleic Acids Res. 28:1397-1406(2000)
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MEDLINE=99206606; PubMed=10192388;
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                                                                                                                                                                      60984 MW;
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hes 5; Conserv
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          VARSPLIC
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Matches
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                    507
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2ASD_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-New Zealand; TISSUE-Brain, and Skeletal muscle;
MRDLINE-96161994; PubMed=8576224;
CROTTOS C., Zolnierowicz S., Bako E., Durbin S.D., Depaoli-Roach A.A.;
"High complexity in the expression of the B' subunit of protein phosphatase 2A0. Evidence for the existence of at least seven novel
                                                                                                                                                                     Pfam; PF00133; tRNA-synt 1; 1.—PRINTS; PR0141; TRNA-SYNTHMET.
TIGRFAMS; TIGR00398; metG; 1.
PROSITE; PS00178; AA TRNA_IGASE I; FALSE_NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Metal-binding; Zinc; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 271:2578-2588 (1996).
FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC BNZYME TO A PARTICULAR SUBCELLULAR COMPARTMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa CONSTANT REGULATORY SUBUNIT (PR65 or SUBUNIT A), THAT ASSOCIATES WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subunit,
subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _2ASD_RABIT STANDARD; PRT; 586 AA.

Q28653; Q28655;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
26-Indevine protein phosphatease 2A, 56 kDa regulatory subunit delta isoform (PP2A, B subunit, B' delta isoform) (PP2A, B subunit, PR61 delta isoform) (PP2A, B subunit, R8 delta isoform) (PP2A, B subunit, R8 delta isoform) (PP2A, B subunit, R8 delta isoform) (PP2A, B subunit, B1-gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 1; Length 551; 100.0%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                          CAB2E383314E2B19 CRC64;
                                                                                                                                                                                                                                            "HIGH" REGION.
"KMSKG" REGION.
ATP (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
D -> G (IN REF. 1).
V -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                 InterPro; IPR002300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt I.
InterPro; IPR002304; tRNA-synt met.
                                                         EMBL; AE001598; AAD18275.1; -. EMBL; AE002223; AAF38466.1; -. EMBL; AP002545; BAA98333.1; -. HSSP; PO0959; IMEA. PHCI-2DPAGE; Q92959; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                          63453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                       333
144
147
157
160
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147
157
160
171
171
551 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 EILDV 533
                                                                                                                      TIGR; CP0651;
                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                1 EILDV
                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                  METAL
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WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56 FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS, AND CELL SIGNALING MOLECULES.
-!- SUBCELLULAR LOCATION NUClear (By similarity).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3 BINDING, CLASS I (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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that target PP2A to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multigene family, Nuclear protein, Repeat.
DOMAIN 21 36 8 X 2 AA APPROXIMATE TANDEM REPEATS OF
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Q14736; O00696; O00494; Q15171;
30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Serine/threconine protein phosphatese 2A, 56 kDa regulatory subunit,
delta isoform (PP2A, B subunit, B' delta isoform) (PP2A, B subunit,
B56 delta isoform) (PP2A, B subunit, PR61 delta isoform) (PP2A, B subunit,
R5 delta isoform) (PP2A, B subunit, PR61 delta isoform) (PP2A, B
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MEDLINE=97324098; PubMed=9180267;
MIDALON, GOMEZ G.A., Nishito Y., Usui H., Takeda M.;
Manabe O., Gomez G.A., Nishito Y., Usui H., Takeda M.;
"Molecular heterogeneity of the cDNA encoding a 74-kba regulatory subunit (B'' or delta) of human protein phosphatase 2A.";
FEBS Lett. 408:52-56(1997).
                                                                                                                                                                                                                                                                                                                                                           CAUTION: NOMENCLATURE USED IN REF.1 REFERS TO PP2A B SUBUNIT B' GAMMA ISOFORM, WHICH IS CITED AS PP2A B SUBUNIT DELTA-PR61 ISOFORM IN LATER PUBLICATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68090 MW; E149A309CDDA7495 CRC64;
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TISSUE=Fetal brain;
MEDLINE=96355607; PubMed=8703017;
MCIGHT B., Rivers A.M., Audlin S., Virshup D.M.;
"The B56 family of protein phosphatase 2A (PP2A) reguencodes differentiation-induced phosphoproteins that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS DELTA-1 AND DELTA-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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J. Biol. Chem. 271:22081-22089(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U38193; AAC48532.1; -. EMBL; U38195; AAC48534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
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386 EILDV 390

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBURITY PRA CONSISTS OF A COMMON HETBRODIMERIC CORE ENZYME, COMPOSED OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATES WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS PAMILLES), THE 48 KDA VARIABLE REGULATORY SUBUNITY, VIRAL PROTEINS, AND CELL SIGNALING MOLECULES.
SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR IN INTERPHASE, NUCLEAR DURING MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Substraint of the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. -!- PUNCTION: THE B REGULATORY SUBMIT MIGHT MODULATE SIBLECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3 BINDING, CLASS I (POTENTIAL),
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL),
MISSING (IN ISOFORM DELTA-3),
MISSING (IN ISOFORM DELTA-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: 3 ISOFORMS, DELTA-1 (SHOWN HERE), DELTA-2 AND DELTA-3, ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ISOFORM DELTA-2 IS WIDELY EXPRESSED. ISOFORM DELTA-1 IS HIGHLY EXPRESSED IN BRAIN.
INDUCTION: BY RETINOTC ACID; IN NEUROBLASTOMA CELL LINES.
PTM: AT LEAST ISOFORM DELTA-1 IS PHOSPHORYLATED ON SERINE
                            SEQUENCE FROM N.A. (ISOFORM DELTA-2), AND SEQUENCE OF 501-508; 550-559; 573-580 AND 584-601 (DELTA-1).
TISSUE-Brain cortex, and Bone marrow;
MEDLINE-96159032; PubMed-8566219;
Tanabe O., Nagase T., Murakami T., Nozaki H., Usul H., Nishito Y., Hayashi H., Kagamiyama H., Takeda M.;
"Molecular cloning of a 74-kDa regulatory subunit (B'' or delta) of FEBS Lett. 379:107-111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 X 2 AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Phosphorylation; Alternative splicing; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F15F71AF4E565387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS DELTA-1 AND DELTA-2) IISSUE-Colon, Bye, and Kidney;
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548 565 NUQ
11 116 MIS
85 116 MIS
602 AA; 69991 NW; 1
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EMBL; BC001175; AAH01175.1; -.
EMBL; BC010692; AAH10692.1; -.
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EMBL; AB000634; BAA20381.1; -.
EMBL; AB000635; BAA20382.1; -.
EMBL; D78360; BAA11372.1; -.
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InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
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VARSPLIC
SEQUENCE
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                      Gaps
                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
TOPA OR BH2467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TICRFAMS; TICRO1051; topA bact; 1.
PROSITE; PS00196; TOPOISOMERASE I PROK; 1.
Isomerase; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA CLEAVAGE (BY SIMILARITY).
                                                                                                                                    Bacillus halodurans.
Bacteria, Firmicutes; Bacillales; Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EE3E9EE0B5546256 CRC64;
                           690 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002936; DNAprim toprim.
InterPro; IPR003601; DNAtopI_ATP bind.
InterPro; IPR003601; DNAtopI_DNA_Bind.
InterPro; IPR0003602; DNAtopI_DNA_Bind.
InterPro; IPR0003602; Drok tplsomrase.
Pfam; PP01131; Topoisom_bac; 1.
Pfam; PP01301; Drok in: 1.
PRINTS; PR00417; PRTPISMRASEI.
SWART; SM00437; TOPIBC; 1.
SWART; SM00493; TOPIBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C4-TYPE 1.
C4-TYPE 2.
C4-TYPE 3.
                                                                                                                                                                                                                         MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP001515; BAB06186.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78910 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                           STANDARD;
                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           690 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P06612; 1ECL
                                                                                                                                                                NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAMILY.
                          TOP1 BACHD
Q9KAZ3;
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ACT_SITE
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RESULT 51
TOP1_BACHD
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Gaps

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0; Indels

0; Mismatches

5; Conservative

Best Local Similarity

Query Match

100.0%; Score 23; DB 1; Length 602; 100.0%; Pred. No. 3.3e+02;

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1 EILDV 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constituents.
                                                                                                                                                                                                                                                                                       BOVIN
                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                T 54
BOVIN
                                                                                                                                                                              Matches
SSSSSSSSSEES
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                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                               MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulman B.R., Lu Z., Zeak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
"The genome of fowlpox virus.";
-!- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS
ASSOCIATED WITH VETF:
-!- SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley; TISSUE=Brain; MEDLINE=97073413; Pubméd=8915891; Neutre=97073143; Pubméd=8915891; Neutre-Jehle M., Denizot J.P., Borbely A.A., Mallet J.; Characterization and sleep deprivation-induced expression modulation of dendrin, a novel dendritic protein in rat brain neurons."; J. Neurosci. Res. 46:138-151(1996).
-i. MISCELLANEOUS: MODULATED BY SLEEP DEPRIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                            Fowlpox virus (FPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Early transcription factor 82 kDa subunit (VETF large subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 1; Length 709; 100.0%; Pred. No. 4e+02; vive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Activator.
SEQUENCE 709 AA; 82729 MW; 79C39E93A84E051C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Dendrin (Fragment)
                                                                                             709 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       719 AA
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF198100; AAF44515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.03
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                               NCBI_TaxID=10261;
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                                 519 EILDV 523
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                                                                                                                                                                                                     Avipoxvirus
         1 EILDV
                                                                                            ETF2 FOWPV
Q9J562;
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P50617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cooperates with MD-2 and TLR6 to mediate the innate immune response to bacterial lipoproteins and other microbial cell wall components. Acts via MyD88 and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response. May also promote apoptosis in response to lipoproteins (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guionaud C.T., Dubey C., Zumkehr J.R., Sonstegard T.S., Jungi T.W., "Role of bovine TLR2, TLR4 and CD14 in the recognition of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 719; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Immune response; Inflammatory response; Signal;
                                                                                                                                                                                                                                                                                                                                                            719 AA; 77208 MW; 89E2ED094514EAFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95LA9; Q9GL66;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR Cterm.
InterPro; IPR000157; TIR_domain.
Pfam; PP00560; LRR; G.
Pfam; PP01463; LRRCT; 1.
Pfam; PP01582; TIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foll-like receptor 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF368419; AAL16722.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF310951; AAG32060.1; -.
                                                                                                                                                                                                                                                                                          EMBL; X96589; CAA65407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MEDLINE=98421677; PubMed=9751057;
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SIGNAL
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MEDLINE-98261424; PubMed=9596645;
Chaudhary P.M., Ferguson C., Nguyen V., Nguyen O., Massa H.F., Eby M., Jasmin A., Trask B.J., Hood L., Nelson P.S.,
Cloning and characterization of two Toll/Interleukin-1 receptor-like genes Till and Tile: evidence for a multi-gene receptor family in
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              060603; 015454; Created)
15-UNA-2002 (Rel. 41, Last sequence update)
15-UNA-2002 (Rel. 41, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Toll-like receptor 2 precursor (Toll/interleukin 1 receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bazan J.F.
Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 1; Length 784;
Pred. No. 4.4e+02;
Leucine-rich repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    59FDB9DFA7984C18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND RESPONSE TO LIPOPOLYSACCHARIDE
                             TOLL-LIKE RECEPTOR 2.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98118556; PubMed=9435236;
Rock P.L., Hardiman G., Timans J.C., Kastelein R.A.,
A family of human receptors structurally related to
                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998)
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ilarity 100.0%;
Conservative 0
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  Repeat;
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TLR2 OR TIL4.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                    442
784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
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 Transmembrane;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 EİLDV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EILDV 5
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CARBOHYD
CARBOHYD
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DOMAIN
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SEQUENCE
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A Goddard, N. Wood W. I., Gurney A., Huang A., Xie M. H., Zhang M.,

R. Toll-like receptor 2 mediates lipopolysaccharide-induced cellular

R. Signalling.

R. Mingel G. W. Wood W. I., Gurney A., G., Godowki P. J.;

R. Mingel G. W. Godowki P. J., Godowki P. J.

R. Mingel G. W. Godowki P. J. Signible Hrough

R. Milpense 1981:786-719 [1999].

R. Milpense 1981:786-719 [1999].

R. Milpense 1981:786-719 [1999].

R. Milpense 1981:786-719 [1999].

R. Science 2861:786-719 [1999].

R. W. Y. Tao X., Ban B., Hong T., Medshittov R., Manlay JL., Tong L.;

R. W. Y. Tao X., Shan B., Hong T., Medshittov R., Manlay JL., Tong L.;

R. Structural basis for signal transduction by the Toll/interleukin.1

R. Structural basis for signal transduction by the Toll/interleukin.1

R. Structural basis for signal transduction by the Toll/interleukin.1

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EMBL; AB020807; BAA78631.1; -.
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Genew, HGNC:16711, TLR6.
MIM, 605403, -.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
P->F ABOLISHES THE INTERACTION WITH
MYD88 NO EFFECT ON OLIGOMERIZATION ON THE STRUCTURE OF THE TIR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bulut Y., Faure E., Thomas L., Equils O., Arditi M.,
"Cooperation of Toll-like receptor 2 and 6 for cellular activation 1 soluble tuberculosis factor and Borrelia burgdorferi outer surface protein A lipoprotein: role of Toll-interacting protein and IL-1 receptor signaling molecules in Toll-like receptor 2 signaling "; J. Immunol. 167:997-994(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Participates in the innate immune response to Grampositive bacteria and fungi. Acts via MyD88 and TRAF6, leading to Desitive bacteria and fungi. Acts via MyD88 and TRAF6, leading to Trappara activation. To tytokine secretion and the inflammatory response. Recognizes mycoplasmal macrophage-activating lipopeptide-2kD (MALP-2), soluble tuberculosis factor (STF), phenol soluble modulin (FSM) and B.burgdorferi outer surface protein A lipoprotein (OSPA-L) cooperatively with TLR2. SUBUNIT: Binds TLR2 via their respective extracellular domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Placenta;
MEDLINE=99250250; PubMed=10231569;
MEDLINE=99250250: PubMed=10231569;
MEDLINE=99250250: Takeuchi O., Kawai T., Sanjo H., Copeland N.G., Gilbert D.J.,
Jenkins N.A., Takeda K., Akira S.;
"TLR6: A novel member of an expanding Toll-like receptor family.";
Gene 231:59-65(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                        (POTENTIAL)
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7DBE6B24CF1FAF8B CRC64;
CYTOPLASMIC (POTENTIAL)
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ID TLRG HUMAN STANDARD; PRT; 796 AA. AC. 03Y2C9;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Toll-like receptor 6 precursor.
                                                                                                                                                                                                                                                                          0; Mismatches
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                            89837 MW;
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Best Local Similarity
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784 AA;
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Binds MyD88 via their respective TIR domains (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and phagosomes (By similarity).

-!- TISSUE SPECIFICITY: Detected in monocytes, CD11c+ immature dendritic cells, plasmacytoid pre-dendritic cells and dermal microvessel endothelial cells.

-!- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.

-!- SIMILARITY: CONTAINS 1 TIR DOMAIN.

-!- SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leucine-rich repeat; Glycoprotein.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; I
100.0%; Pred. No. 4.5e+02;
iive 0; Mismatches 0;
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InterPro; IPR00483; LRR_Cterm.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000157; TIR_domain.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
PRINTS; PR00019; LEURICHPPT.
SMART; SM00370; LRR; 2.
SMART; SM000255; TIR; 1.
PROSITE; PS50104; TIR; 1.
PROSITE; PS50104; TIR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spirochete.";
Science 281:375-388(1998).
-!- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS IN
PRESENCE OF ATP. HYDROLYZES TWO ATPS FOR EACH PEPTIDE BOND CLEAVED
IN THE PROTEINS UBSTRATE (BY SIMILIARITY).
-!- CATALYTIC ACTIVITY: HYDROLYSES Of large protesins such as globin,
casein and denaturated serum albumin, in presence of ATP.
-!- SUBDINT: HONOTERPARER (BY SYMILIARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY $16.
                                                                                                                                                                                                                                                  STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                            Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
                                                           30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATF-dependent protease La (EC 3.4.21.53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001227; AAC65510.1; -.
                                       30-MAY-2000 (Rel. 39, Created)
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                                                                                                                                                                                                                                                                                                                                                HISSUE 98330437; PubMed=9664034; Marke P.W., Arai M., Bandura J.L., Kwiatkowski D.J.; Marke P.W., Arai M., Bandura J.L., Kwiatkowski D.J.; Marke P.W., Arai M., Bandura J.L., Kwiatkowski D.J.; Addillin (1992): a new member of the gelsolin/villin family of actin regulatory proteins...,
J. Call Sci. 111:2129-2136(1998).
J. Call Sci. 111:2129-2136(1998).
I Call Sci. 111:2129-2136(1998).
I Call Sci. 111:2129-2136(1998).
J. Call Sci. 111:2129-2136(1998).
I CALL SCI ARGURITY: MOST HIGHLY EXPRESSION ALSO DETECTED IN THE THYMUS, PROSTATE. TESTES AND UTERUS.
PROSTATE. TESTES AND UTERUS.
--- SIMILARITY: CONTAINS 6 GELSOLIN-LIKE REPEATS.
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                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In-binding, Capping protein; Repeat.

CORE (BY SIMILARITY).

HEADPIECE (BY SIMILARITY).

GELSOLIN-LIKE 1.

GELSOLIN-LIKE 2.

GELSOLIN-LIKE 3.

GELSOLIN-LIKE 4.

GELSOLIN-LIKE 5.

GELSOLIN-LIKE 6.

VHP.

POLYPHOSPHOINOSITIDE BINDING (BY SIMILARITY).
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                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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InterPro; 1PR001974; Gelsolin.
InterPro; 1PR0013128; VHP.
Pfam; PP00658; Gelsolin; 6.
Pfam; PP02209; VHP; 1.
SMART; SM00262; GEL; 6.
SMART; SM00153; VHP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF041449; AAC25051.1; -.
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DOMAIN 1 731
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                                                             STANDARD;
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                                                                                                                                                                  Advillin (p92).
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                                                           ADVL HUMAN
075366;
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR003959; AAA—ATPase cen
InterPro; IPR001270; Chaprnin_clpA/
InterPro; IPR001311; LON.
InterPro; IPR001311; LON.
InterPro; IPR004915; Lon_fam.
Pfam; PP000004; AAA; 1.
Pfam; PP000004; AAA; 1.
Pfam; PP001000; CuPPROTEASEA.
PRINTS; PR00300; CuPPROTEASEA.
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Matches

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Matches
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RNE_BUCAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92052220; PubMed=1946430;
A Kaptain S., Downey W.E., Tang C.K., Philpott C., Haile D.J.,
A Orloff D.G., Harford J.B., Rouault T.A., Klausner R.D.;
A Orloff D.G., Harford J.B., Rouault T.A., Klausner R.D.;
A Orloff D.G., Harford J.B., Rouault T.A., Klausner R.D.;
Droc. Natl. Acad. Sci. U.S.A. 88:10109-10113(1991).
-!- FUNCTION: BINDS TO IRON RESPONSIVE ELEMENTS (IRES), WHICH ARE STEM-LOOP STRUCTURES FOUND IN THE S'UTR OF PERRITIN, AND DELTA ANINOLEVULINIC ACID SYNTHASE MRNAS, AND IN THE 3'UTR OF TRANSFERRIN RECEPTOR MRNA. BINDING TO THE IRE ELEMENT IN PERRITIN RECULT TO THE TRANSFERRIN RECEPTOR MRNA INHIBITS THE DEGRADATION OF THIS OTHERWISE RAPIDLY DEGRADED MRNA.
-- CHALVITON: THIS PROPERIN ALSO EXPRESSES ACONITASE ACTIVITY.
-- CATALYTIC ACTIVITY: Citrate = cis-aconitate + H(2)O.
-- SUMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                   TERL HUMAN STANDARD; PRT; 889 AA.
P21399; Q14652;
01-MAY-1991 (Rel. 18, Created)
15-JUJ-1998 (Rel. 36, Last sequence update)
15-JUJ-1998 (Rel. 31, Last annotation update)
15-JUJ-1998 (Rel. 31, Last annotation update)
15-JUJ-1998 (Rel. 31, Last annotation update)
15-JUJ-1998 (Rel. 31, Last annotation update)
15-JUJ-1998 (Rel. 31, Last annotation update)
16-JUJ-1998 (Rel. 31, Last annotation update)
17-JUJ-1998 (Rel. 31, Last annotation update)
18-JUJ-1998 (Rel. 31, Last annotati
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Expression of active iron regulatory factor from a full-length human cDNA by in vitro transcription/translation."; Nucleic Acids Res. 20:33-39(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 53-889 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=91045916; PubMed=2172968;
Rouault T.A., Tang C.K., Kaptain S., Burgess W.H., Haile D.J.,
Samaniego F., McEridd O.W., Harford J.B., Klausner R.D.;
"Cloning of the cDNA encoding an RNA regulatory protein -- the human
iron-responsive element-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 87:7958-7962(1990).
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92150156; PubMed=1738601;
Hitling H., Emery-Goodman A., Thompson N., Neupert B., Seiser C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hentze M.W., Argos P.,
"Homology between IRE-BP, a regulatory RNA-binding protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY TO ACONITASES AND IPM ISOMERASES.
MEDLINE=91232935; PubMed=1903202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aconitase, and isopropylmalate isomerase.";
Nucleic Acids Res. 19:1739-1740(1991).
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EMBL; BC018103; AAH18103.1; -
EMBL; M58510; AAA69900.1; -.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                               Kuehn L.;
                     IRE1_HUMAN
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-i- SUBUNIT: ORGANIZED INTO A STRUCTURE (PROCESSOME OR RNA DEGRADOSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLVKKODIENILHWNVTQH -> CPRKTRTQNLPPWLSNKL
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STRAIN=TOkyo 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
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                                                                           InterPro; IEI.

InterPro; IPR001030; Acc...

R Pfam; PF001054; Aconitase; 1.

R PRINTS; PR00415; ACONITASE.

DR PROSITE; PS00456; ACONITASE 1; 1.

PROSITE; PS01244; ACONITASE 1; 1.

DR PROSITE; PS01244; ACONITASE 2; 1.

DR PROSITE; PS01244; ACONITASE 2; 1.

DR PROSITE; PS01244; ACONITASE 2; 1.

TRON-SULFUR (4FE-4S; RNA-VETAL 437 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187 SIM 187
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E1A05AF701D46DCB CRC64;
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-!- SIMILARITY: BELONGS TO THE RNE FAMILY.
-!- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.
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Bacteria; Proteobacteria; gamma subdivision; Buchnera.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ribonuclease E (EC 3.1.4.-) (RNase E)
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Genew, HGNC:117; ACO1.
MIM; 100880; --
InterPro; IPR000573; Aconitase C.
InterPro; IPR01030; Aconitase N.
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SMART; SM00316; S1; 1.
TIGRFAMS; TIGR00757; RNaseEG; 1.
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InterPro; IPR004659; RNaseEG.
InterPro; IPR003029; S1.
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Best Local Similarity
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Conservative
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                                                                                      RESULT 62
HEPA HAEIN
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  Matches
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                                                                                       ö
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Engelender S., Kaminsky Z., Guo X., Sharp A.H., Amaravi R.K., Kleiderlein J.J., Margolis R.L., Troncoso J.C., Lanahan A., Worley P.F., Dawson V.L., Dawson T.M., Ross C.A.; Symphilin-1 associates with alpha-synuclein and promotes the formation of cytosolic inclusions."; Nat. Genet. 22:110-114(1999).

-I. SUBUNIT ASSOCIATES WITH SNCA.

-I. TISSUB SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN BRAIN, HEART AND PLACENTA.

-I. MISCELLANEOUS: CONSTRUCTS ENCODING PORTIONS OF SNCA AND SCNCAIP CO-TRANSPECTED IN MAMMALIAN CELLS PROMOTE CYTOSOLIC INCLUSIONS RESEMBLING THE LEWY BODIES OF PARKINSON DISEASE.
PROSITE; PS50126; S1; 1.
Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome.
DOMAIN 39 119 S1 MOTIF.
                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 1; Length 919; 100.0%; Pred. No. 5.2e+02;
                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 ANK 5 (POTENTIAL).
729 ANK 6 (POTENTIAL).
100380 MW; 5CE0022E0024EEA4 CRC64;
                        DÓMAIN 39 119 SI MÓTIF.
SEQUENCE 902 AA; 104006 MW; C3FA00476E3C2E37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SMOUZ48; ANNA, 2.

PROSITE; PSS0089; ANK REPEAT; 1.

PROSITE; PSS0297; ANK REP REGION; 1.

Coiled coil; Repeat; ANK Tepeat.

REPEAT 349 380 ANK 1.

REPEAT 413 ANK 2.

REPEAT 448 ANK 3.

REPEAT 456 485 ANK 4.

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).
                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Symphilin 1 (Alpha-symuclein interacting protein).
                                                            / Match 100.0%; Score 23; DB 1; I
Local Similarity 100.0%; Pred. No. 5.1e+02;
nes 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                      919 AA
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=99251592; PubMed=10319874;
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF076929; AAD30362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC:11139; SNCAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 603779; -.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 2.
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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515
603
699
7
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                                                                                                                                       525 KILDV 529
                                                                                                               1 BILDV 5
                                                                                                                                                                                                      SYNP HUMAN
                                                              Query Match
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Lu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hannam M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA polymerase associated protein homolog (ATP-dependent helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995).
-!- SUBUNIT: BINDS TO THE RNA POLYMERASE (RNAP) (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SNP2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8022403581DAADBD CRC64;
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                                                                                                                                                                                                  923 AA.
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                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Rd / KW20 / AICC 51907;
MEDLINE=95350630; Pubmed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001650; Helicase_C.
InterPro; IPR000330; SNF2_N.
Pfam; PP00176; SNF2_N; 1.
Pfam; PP00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104405 MW;
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1 / KW20 / ATCC 51907;
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TIGR; HI0616; -.
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Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=727;
                                                   152 EILDV 156
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ID GLND_RHIME
AC P56884;
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MEDLINE-2003488; PubMed=10617198;

MEDLINE-2003488; PubMed=10617198;

MAPLY K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

MARTIS B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

Meichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

Meichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

Kreis M., Delseny M., Pugdomench P., Watson M., Schmidtheini T.,

Reichert B., Portetelle D., Perez-Alonso M., Bancroft I.,

Nos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Bliham L., Robben J.,

Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

Braeken M., Weltjens I., Voet M., Bastieans I., Aert R., Defoor E.,

Weitzenegger T., Bothe G., Rampsperger U., Hilbert H., Braun M.,

Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,

Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Van den Daele H.,

Berneiser S., Hempel S., Feldelmusch M., Lamberth S., Van den Daele H.,

De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercg R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Preprotein translocase seck subunit, chloroplast precursor.
SECA OR AT4G01800 OR T7811.6.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                          Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 1; Length 952; 100.0%; Pred. No. 5.4e+02; cive 0; Mismatches 0; Indels
   Hypothetical 105.3 kDa protein C01G6.5 in chromosome III
                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 FHA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 100 FHA.
952 AA; 105274 MW; D9CFB0AB3C685FBE CRC64;
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WormPep, C01G6.5, CE00867,
InterPro, IPR000253, FHA_domain.
Pfan, PF00498, FHA, 1...
SMART, SM00240, FHA, 1...
PROSITE, PS50006, FHA_DOMAIN, 1...
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                                                                         Caenorhabditis elegans.
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Q9SYI0;
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SECA_ARATH
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE 21396507; PubMed=11481430; Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Bosteard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont sinorhizobium meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A, 98:3977-9882(2001).
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
15-UDN-2002 (Rel. 41, Last annotation update)
[Protein-PII] uridylyltransferase (EC 2.7.59) (PII uridylyl-
transferase) (Uridylyl removing enzyme) (UTase).
GLND OR R00396 OR SWC01124.
Rhizobium meliloti (Sinorhizobium meliloti).
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rudnick P.A., Arcondeguy T., Kennedy C.K., Kahn D.; "glnD and mviN are genes of an essential operon in Sinorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase, Nucleotidyltransferase, Nitrogen fixation,
Complete proteome.
SEQUENCE 949 AA; 106381 MW; EF549C1B0D8540A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE GLND FAMILY.
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InterPro; IPR003607; MB Pplase HDC.
InterPro; IPR002934; NTP_transf.
Pfam; PF01904; ACT; 2.
Pfam; PF01909; NTP_transf_2; 1.
Pfam; PF01906; HD; 1.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21172888; Pubmed=11274131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 183:2682-2685(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF227730; AAF37852.1; -. EMBL; AL591783; CAC41833.1; -. InterPro; IPR002912; ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [protein-PII]
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=382;
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01-NOV-1995
01-NOV-1995
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RESULT 64
YKIS_CAEEL
ID YKIS_C.
AC P46012
DT 01-NOV
DT 01-NOV

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Gaps

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CHAINS (BY SIMILARITY)

-!- SUBCELLULAR LOCATION: CONCENTRATED IN THE CELL BODY OF THE NEURONS, PARTICULARLY IN THE PERINUCLEAR REGION.
-!- DOMAIN: COMPOSED OF THEE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH INTERACTS WITH OTHER PROFELIES: (SUCH AS THE KINESIN LIGHT CHAINS), VESICLES AND MEMBRANOUS ORGANELLES.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
                                                                                                                                                                                                                                                                               MEDLINE-99000842; PubMed-9782088;
Xia C., Rahman A., Yang Z., Goldstein L.S.B.;
"Chromosomal localization reveals three kinesin heavy chain genes in
          01-OCT-1993 (Rel. 27, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuronal kinesin heavy chain (NKHC) (Kinesin heavy chain isoform 5A)
(Kinesin heavy chain neuron-specific 1).
KIRS NES ON NKHC1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Cell Biol. 119:1287-1296(1992).
-!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M.,
Hirokawa N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Kinesin family in murine central nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=93077686; PubMed=1447303;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 89-231 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   Genomics 52:209-213(1998).
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                  mouse.
              Van Montagu M., Rogers J., Cronin A., Quail, M., Bray-Allen S.,
Ratetet A., Rajandream M.A., Lyne M., Benes V., Rechamn S.,
Rettett D., Boggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
Ra Borkova D., Bloecker H., Scharfe M., Benes V., Rechamn S.,
Borkova D., Bloecker H., Scharfe M., Granderath K., Loehnort T.-H.
Ra Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
Ra Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
Ra Chefdor F., Cooke R., Berger C., Monford M., Bargues M., Terol J., Torres A.,
Ra Chefdor F., Cooke R., Berger C., Monford M., Terol J., Torres A.,
Ra Chefdor F., Cooke R., Berger C., Monford M., Terol J., Torres A.,
Ratishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
Ratishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
Raccaris P., Bevan M., Wilson R.K., Me la Bastide M., Habermann K.,
Raccaris P., Bevan M., Wilson R.K., Me la Bastide M., Habermann K.,
Raccaris P., Bentley D., Sheet P., Cordes M., Abu-Threideh J.,
Ra Schnon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
Rankin T., Kalicki J., Graves T., Harmon G., Edwards J.,
Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
Ra Latreille P., Curtney L., Cloud J., Abbott A., Scott K., Johnson D.,
Ra Minx P., Bentley D., Pulton B., Miller N., Greco T., Kemp K.,
Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
Rankondu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
Rawby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
Ryanet S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
Ryanet M., Martienssen R., McCombie W.R.;
Ryanet M., Martienssen R., McCombie W.R.;
Ryanet Marra M., Martienssen R., Marcondine W.R.;
Ryanet Marra M., Martienssen R., Marcondine W.R.;
Ryanet Marra M., Martienssen R., McCombie W.R.;
Ryanethan D., Martienssen R., Marcondine W.R.;
Ryanence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein transport, ATP-binding, Chloroplast, Translocation, Transport, Transit peptide. P. CHLOROPLACT (DOMESTALL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLUIAR LOCATION: CHLOROPLAST STROMA. A MINOR FRACTION IS ASSOCIATED WITH THE THYLAKOID MEMBRANE. SIMILARITY: BELONGS TO THE SECA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402:769-777(1999).
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. LIKELY PARTICIPATES IN PROTEIN TRANSLOCATION ACROSS THE THYLAKOID MEMBRANE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLOROPLAST (POTENTIAL).
PREPROTEIN TRANSLOCASE SECA SUBUNIT.
ATP (POTENTIAL).
Wi 3D2AE013DB347187 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 1021; 100.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 183 ATP
1021 AA; 115114 MW;
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Pfam; PF01043; Seca protein; 1.
PRINTS; PR00906; SECA.
TIGRFAMS; TIGR00963; seca; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC007138; AAD22642.1; -.
EMBL; AL161492; CAB77750.1; -.
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                                                                                                                                                                                                                                                                                                                         MCD; MCI:LU--

A InterPro; IPR001752; ...

B Fam; PR00225; Kinesin; 1.

DR PRINTS; PR00329; KISC; 1.

DR SMART; SM00129; KISC; 1.

DR ROSITE; PS00671; KINESIN MOTOR DOMAIN1; 1.

DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.

DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.

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TOWAIN SIMILARITY).

MICROTUBULE-BINDING.

TOWAIN SIMILARITY).
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                                                                                                                                                                                                                                                                                                        HSSP, P56536; ZKIN.
MGD; MGI:109564; Kif5a.
InterPro; IPR001752; kinesin_motor.
                                                                                                                                                                                                                                                       EMBL; AF067179; AAC79803.1; -. PIR; C44259; C44259.
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Best Local Similarity
Matches 5; Conserv
SUBFAMILY
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0; Mismatches

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Matches

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PRT; 1027 AA.

STANDARD;

KINN MOUSE
ID KINN MOUSE
AC P33175; Q922F9;

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                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: CONCENTRATED IN THE CELL BODY OF THE NEURONS. PARTICULARLY IN THE PERINUCLEAR REGION.
-1- TISSUE SPECIFICITY: DISTRIBUTED THROUGHOUT THE CNS BUT IS HIGHLY ENRICHED IN SUBSERS OF NEURONS.
-1- DOWAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE NOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMBALZATION, AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS), VESICLES AND MEMBRANOUS ORGANELLES.
                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuronal kinesin heavy chain (NKHC) (Kinesin heavy chain isoform 5A)
(Kinesin heavy chain neuron-specific 1).
                                                                                                                                                                                                                                                 TISSUE-Hippocampus;

BEDLINE-2424242, PubMed-7514426;

Niclas J., Navnor F., Hom-Booher N., Vale R.D.;

"Cloning and localization of a conventional kinesin motor expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                         Neuron 12:1059-1072(1994).
-!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
-!- ROLTON: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
-!- SUBUNII: OLLGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICROTUBULE-BINDING.
ATP (BY SIMILARITY).
W; 04C0C12342020794 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM, 602821; ...
InterPro; IFR001752; kinesin motor.
Pfam: PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117392 MW;
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315
                                                                                                                                                                                                                                                                                               exclusively in neurons.
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86 9
1032 AA;
                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=9606;
                  179 EILDV 183
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EILDV
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MEDLINB=21156211; PubMed=11258796;
MEDLINB=21156211; PubMed=11258796;
MEDLINB=21156211; PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterchemorrhagic Escherichia coli
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
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STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grobbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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EMBL; AP002563; BAB31174.1; -.
InterPro; IPR001450; ¥Fe45_ferredoxin.
InterPro; IPR001327; FAD pyr redox.
InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                       Hypothetical protein ygfK. YGFK OR Z4217 OR ECS3751. Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:529-533(2001).
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                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=83334;
                                                        179 EILDV 183
'n
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15-JUN-2002
                                                                                                                                                                  YGFK ECOS7
ID YGFK ECOS7
AC Q8XD75;
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1 EILDV
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1 EILDV

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Length 1032;

Score 23; DB 1; Pred. No. 5.9e+02;

100.0%;

Query Match Best Local Similarity

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-1- SUBCELLULAR LOCATION: Nuclear (Probable)
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                     CHLOROPLAST.
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SEQUENCE
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DNBI MCMVS
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spinacia oleracea (Spinach).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 1; Length 1032; 100.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Preprotein translocase secA subunit, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               944 944 IRON-SULFUR (4FE-4S) (POTENT
948 948 IRON-SULFUR (4FE-4S) (POTENT
1032 AA, 115581 MW; 588056B51BE89648 CRC64;
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InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR00137; FAT, 1.
Pfam; PF000017; fer4; 1.
ProDom; PD000113; FAD_pyr_redox; 1.
ProDom; P00001139; FAD_pyr_redox; 1.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U28375; AAA83059.1; -.
EMBL; AE000371; AAC75916.1; -.
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1.25 Si Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
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  267 EILDV 271
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Q36795;
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                                                                             RESULT 69
TO YGFK ECOLE
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AC 036795
DT 01-NOV
DT 15-JUN
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PROSITE; PS01312; SECA; 1.
Protein transport; ATP-binding; Chloroplast; Translocation; Transport; Transit peptide.
Transit peptide.
1 776 CHLOROPLAST (DOTTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                            Berghoefer J., Karnauchov I., Herrmann R.G., Kloesgen R.B., "Isolation and characterization of a cDNA encoding the SecA protein from spinach chloroplasts. Evidence for azide resistance of Sec-dependent protein translocation across thylakoid membranes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93033129; PubMed=1329325; Messerle M., Keil G.M., Schneider K., Koszinowski U.H.; Meil G.M., Schneider K., Koszinowski U.H.; Characterization of the murine cytomegalovirus genes encoding the major DNA binding protein and the ICP18.5 homolog."; Virology 191:355-367(1992).

-i- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: CHLOROPLAST STROMA. A MINOR FRACTION IS ASSOCIATED WITH THE THYLAKOID MEMBRANE. -!- SIMILARITY: BELONGS TO THE SECA PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 270:18341-18346 (1995).
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. LIKELY PARTICIPATES IN
PROTEIN TRANSLOCATION ACROSS THE THYLAKOID MEMBRANE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 CHLOROPLAST (POTENTIAL).
36 PREPROTEIN TRANSLOCASE SECA SUBUNIT
37 AT (POTENTIAL).
38 AT (23920878BA93283 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine cytomegalovirus (strain Smith).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230672;
01-ARR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Major DNA-binding protein (MDBP).
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                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-cv. Monatol; TISSUE-Leaf;
MEDLINE-95355455; PubMed-7629156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR000185; SecA.
Pfam; PF01043; SecA protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z49124; CAA88933.1; -.
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1036
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SEQUENCE FROM N.A.
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MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
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Totivation requires a sequential transfer of a phosphate proup from a His in the primary transmitter domain, to a Asp in the receiver domain and to a His in the secondary transmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
 SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                                                                                               100.0%; Score 23; DB 1; Length 1191; 100.0%; Pred. No. 6.9e+02;
                                                                                                                                                                              Pfam; PF00747; viral DNA bp; 1.
DNA-binding; DNA replication; Zinc-finger; Nuclear protein;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                   1191 AA; 131640 MW; 5BA4A7F07D7E1B9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1197 AA
                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                          C2HC-TYPE
                                                                                                                                         EMBL; X67021; CAA47414.1; -. PIR; A44051; A44051. InterProj. IPR000635; Viral_DNA_bind.
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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ZN FING 47
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HISTIDINE KINASE.
RESPONSE REGULATORY.
SECONDARY TRANSMITTER DOMAIN (POTENTIAL).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Escherichia.
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Pred. No. 7e+02;
; Mismatches 0; Indels (
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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BY 10855; P77644; Q9RF36; Q9RF37;

O1-JUL-1993 (Rel. 26, Created)

O1-NOV-1997 (Rel. 35, Last sequence update)

15-JUN - 2002 (Rel. 41, Last annotation update)

Sensor protein evg8 precursor (EC 2.7.3.-).

EVGS OR B2370.
                                                                                                                                                                                                                                           EMBL, ABO02561; BAB36672.1; ...
InterPro; IPR004359; HIS KIN eig.
InterPro; IPR004359; HIS KIN eig.
InterPro; IPR004359; HIS KIN eig.
InterPro; IPR004361; Hig kinā.
InterPro; IPR001361; Hpt.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001638; SBP_bac_3.
InterPro; IPR001638; SBP_bac_3.
InterPro; IPR001638; SBP_bac_3.
InterPro; IPR001638; HaTPase c; 1.
SWART; SW00073; HPT; 1.
SWART; SW00062; PBPb; 2.
SWART; SW0062; PBPb; 2.
SWART; SW0062; PBPb; 2.
SWART; SW0062; PBPb; 2.
SWART; SW00649; HIS KIN; 1.
PROSITE; PS50110; RESPONSE REGILATORY; 1.
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CHAIN 22 1197
DOWAIN 22 325
TRANSMEM 326 346
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RPOD_SYNY3

ID _RPOD_SYNY3 STANDARD; PRT; 1317 AA

AC P73374;
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                          interPro; 1FR002570; Hpt.
InterPro; 1PR001789; Response reg.
InterPro; IPR001111; SBP/glu receptor.
InterPro; IPR001638; SBP_bac_3.
InterPro; IPR001638; SBP_bac_3.
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                                                          EMBL, AF201840; AAF17563.1; --
EMBL, AF201841; AF47564.1; --
EMBL, AE000325, AAC76429.1; --
EMBL, D90867; BAA16241.1; --
EMBL, D90867; BAA16241.1; --
HSSP; P06143; 1UD21.
HSSP; P06143; 1UDR.
EcoGene; EG11610; evgS.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003594; HIS KIN Big.
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00072; response reg;
Pfam; PF00497; SBP bac 3; 1.
Pfam; PF00512; signal; 1.
Pfam; PF02518; HATPase_c; 1.
                                         EMBL; D14008; BAA03108.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97349980; PubMed=9205837; MEDLINE=97349980; PubMed=9205837; MEDLINE=97349980; PubMed=9205837; MEDLINE=97349980; PubMed=9205837; Makine Y., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuthi T., "Construction of a contiguous 874-kb sequence of the Escherichia coli-Kla genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98194702; PubMed-9535079;
Perraud A.-L., Kimmel B., Weiss V., Gross R.;
Perraud A.-L., Kimmel B., Weiss V., Gross R.;
"Specificity of the BvgAs and BvgAs phosphorelay is mediated by the C-terminal HPt domains of the sensor proteins.";
Mol. Microbhol. 27:875-887 (1998).
-I- FUNCTION: Member of the two-component regulatory system evgS/evgA.
Phosphorylates evgA via a four-step phosphorelay in response to
                                                                                                                                                                                                                                                        "Cloning and sequence analysis of the evgAS genes involved in signal transduction of Escherichia coli K-12.";
Nucleic Acids Symp. Ser. 27:149-150(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Probable).

PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to a Asp in the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.K., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Garegor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   environmental signals.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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                                                                                                                                                                                                                   Jtsumi R., Katayama S., Ikeda M., Igaki S., Nakagawa H., Miwa A.,
Taniguchi M., Noda M.;
STRAIN=K12;

MEDLLINE=94171083; PubMed=8125343;

Utsumi R., Katayama S., Taniguchi M., Horie T., Ikeda M., Igaki :
Nakagawa H., Miwa A., Tanabe H., Noda M.;

"Newly, identifiaed genes involved in the signal transduction of
Escherichia coli K-12.";

Gene 140:73-77(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (VARIANTS EVGS1 AND EVGS4).
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                                                                                                                                                                                                  MEDLINE=93173621; PubMed=1289796;
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100.0%; Pred. No. 7e+02;
tive 0; Mismatches 0; Indels (
CYTOPLASMIC (POTENTIAL).
HISTIDINE KINASE.
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CYTOPLASMIC (POTENTIAL)
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                                                                                               SEQUENCE FROM N.A.

MEDLINE=97061201; PubMed=8905231;

Managaina N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,

Okumura S., Shimpo S., Takenchi C., Wada T., Watanabe A.,

Yamada M., Yasuda M., Tabata S.,

"Sequence analysis of the genome of the unicellular cyanobacterium

Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";

DNA Res. 3:109-116(1996).

I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
15-UNA polymerase II large subunit (EC 2.7.7.7) (Pol II) [Contains: Hsp-NRC1 polc intein (Hsp-NRC1 pol2 intein)].
POLC OR POLAZ OR VNG2338G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                         SUBUNIT: IN CYANOBACTERIA THE RNA POLYMERASE IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA, GAMMA, AND DELTA.
                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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MEDLINE=20504483; PubMed=11016950;
NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 100.0%; Score 23; DB 1; Length 1317; Local Similarity 100.0%; Pred. No. 7.7e+02; hes 5; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00623; RNA_pol_A; 1.-
Pfam; PF01854; RNA_pol_A2; 2.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1317 AA; 144776 MW; 27B6970469E7E551 CRC64;
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Halobacteriaceae, Halobacterium.
NCBI_TaxID=64091,
                                                          Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase delta chain (EC 2.7.7.6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                           (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halobacterium sp. (strain NRC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000722; RNA pol A. InterPro; IPR002879; RNA pol A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D90905; BAA17364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
SEQUENCE 1317 AA
                                            Synechocystis sp.
                             OR SLL1789
                                                                   NCBI_TaxID=1148;
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DP2L HALN1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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2ND PART
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SMORDS, HINTN; 1.
INGREMAS, TIGROD354; polC; 1.
PROSITE; PS50818; INTEIN_C_TER; FALSE_NEG.
PROSITE; PS50817; INTEIN_C_TER; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
Nuclease; Exonuclease; DNA-binding; Multifunctional enzyme;
Nuclease; Exonuclease; DNA-binding; Multifunctional enzyme;
Nuclease; Exonuclease; DNA-binding; Multifunctional enzyme;
Nuclease; Exonuclease; DNA-binding; Multifunctional enzyme;
Nuclease; Exonuclease; DNA polymeRASE II LARGE SUBUNIT, 1ST PAF
(POTENTIAL).

"""" POLC INTEIN (POTENTIAL).

""" NEGE SUBUNIT, 2ND PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN) FOLLOWED BY PEPTIDE LIGATION (POTENTIAL).
SIMILARITY: BELONGS TO THE ARCHAEAL DNA POLYMERASE II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETERODIMER OF A LARGE SUBUNIT AND A SMALL SUBUNIT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: Degradation of single-stranded DNA. It acts progressively in a 3'-to 5'-direction, releasing nucleoside 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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1370 AA; 150295 MW; 07878AA9976790C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE005116; AAG20443.1; — InterPro; IPR003586; Hedgehog hintC. InterPro; IPR003587; Hedgehog_hintN. InterPro; IPR002203; Intein. InterPro; IPR004475; POIC_DP2. SWART; SM00305; HintC; 1. SWART; SM00306; HintN; 1
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Matches 5; Conserv
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us-09-251-073a-16.open.rspt

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Q9C264 neurospora
Q8xi12 clostridium
Q8vmp3 pseudomonas
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(without alignments)
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               GenCore version 5.1,3
(c) 1993 - 2003 Compugen Ltd.
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sp bacteria:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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SEQUENCE FROM N.A. Schulte U., Asjan V., Hoheisel J., Brandt P., Fartmann B., Holland R., Schulte U., Asjan V., Hoheisel J., Brandt G., Mewes H.W., Mannhaupt G., Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                         Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 Irom Japan and CML029 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).

EMBL; AR001651; AAD18834.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB8892.1; "BMBL; AR002547; BAAB88892.1; "BMBL; AR002547; BAAB888892.1; "BMBL; AR002547; BAAB888892.1; "BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BMBL; AR002547; BM
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
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Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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; Pred. No. 3.2e+02;
0; Mismatches 0; Indels
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL513463; CAC28719.2;
InterPro; IPR001901; SecE.
InterPro; IPR004195; SecE_euk_arch.
Pf00584; SecE; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Hypothetical 7.8 kDa protein.
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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TIGRFAMS; TIGR00327; SecE cuk arch; 1.
PROSTTE; PS01067; SECE_SECE1G; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 70 AA; 7809 MW. Enterconstructions
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Similarity 100.0%;
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        Q8ulr6 pyrococcus
Q99mdl cricetulus
Q9r0e0 rattus norv
O86693 mus musculu
Q937y3 edwardsiell
O66448 aquifex aeo
Q8r37 arabidopsis
Q8twg7 methanopyru
Q9d3y6 mus musculu
Q55864 synechocyst
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
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MEDLINE-20181728; PubMed-10715320;
Peltier J. D.B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
Adamska I., van Wijk K.J.;
"Proteomics of the chloroplast: systematic identification and
"rargeting analysis of lumenal and peripheral thylakoid proteins.";
Plant Cell 12:119-34 (2000).
--- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
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MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Unknown protein from 2D-page of thylakoid (SPOT251) (Fragment).
Pisum sativum (Garden pea).
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-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF
PROTEIN IS: 8.5, ITS MW IS: 16.9 KDA.
Chloroplast; Thylakoid membrane.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Mypochetical protein CPn0685.
CPN0685 OR CPJ0685.
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088693
Q937Y3
066448
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Q55864
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Best Local Similarity 100.
Matches 5; Conservative
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                NCBI_TaxID=3888;
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7 EILDV 11
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Arakawa T., Hara A., Rukunishi Y., Konno H., Adachi J., Pukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Aizawa T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Saito R.,
Rochill L., Staubi F., Suutki R., Tomita M., Wagner L., Washio T.,
Raka K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Baka J., Boffelli D., Bojunga N., Carninol P., Me Bonaldo M.P.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Austincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Maxararelli J., Mombarts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whanhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Hayashizaki V.
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MGD; MGI:1923108; 4930568L21Rik.
SEQUENCE 100 AA; 11528 MW; 59CFB27CD19C1112 CRC64;
                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                     Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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100.0%; Pred. No. 4.1e+02;
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable cell division topological specificity factor.
MINE OR CPE2137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003193; BAB81843.1; -.
Cell division; Complete proteome.
SEQUENCE 90 AA; 10128 MW; P881B16F95880ACD CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 10.3 kDa protein.
Pseudomonas putida.
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4930568L21RIK.
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Best Local Similarity
5, Conserve
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=13 / TYPE A;
Pubmed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                            flesh-eater.";
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                 01-OCT_2000 (TrEMBLrel. 15, Created)
01-OCT_2000 (TrEMBLrel. 15, Last sequence update)
01-OCT_2000 (TrEMBLrel. 15, Last sequence update)
01-OCT_2000 (TrEMBLrel. 15, Last annotation update)
Mutant c-kit receptor (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN=BROWN NORWAY; TISSUE=TESTIS;
Gangadharan S., Ali S.;
"RT-PCR generated mRNA transcript from proven infertile Brown Norway
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                                                                                                                                                                                                                                                                                                                                                                                                                                male rat testis.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF228308; AAF69131.1; -.
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116 116 116 116 AA; 12583 MW; 8BDASFB24E2471BC CRC64;
  116 AA.
PRT;
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Kichardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Fleischmann R.D., Quackenbush L., Merenney K., Adams M.D., Loftus B.,

Fleischmen R.P., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                STRAIN=BROWN NORMY: TISSUE=TESTIS;

Gangadharan S., Ali S.;

Gangadharan S., Ali S.;

"RT-PCR generated mRNA transcript from proven infertile Brown Norway male rat testis.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ARV2BAII, ARF69134.1;

EINTERPOS, IPR003605, IG like.

SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 23; DB 11; Length 117; Local Similarity 100.0%; Pred. No. 5.2e+02; les 5; Conservative 0; Mismatches 0; Indels C
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100.0%; Score 23; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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117 AA; 12641 MW; F3FBDC2F1288F378 CRC64;
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119 AA; 14025 MW; 7F75DA993E80C15C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaecta; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UIN-2001 (TrEMBLrel. 17, Last annotation update)
C-kit receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last amnotation update)
Hypothetical protein AF1530.
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EMBL, AE000997, AAB89718.1; -.
TIGR, AF1530; -.
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                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"RT-PCR generated mRNA transcript from proven infertile Brown Norway male rat testis ";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF2233309, AAF69132.1;
Interpro, IPR003600; Ig_like.
SMART; SM00410; IG_like.
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"RT-PCR generated mRNA transcript from proven infertile Brown Norway
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                                                                                                                                                                                                                                                                                                       male rat testis.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 74728307; AAF69130.1;
INTERPOS 150.15 19_11ke.
SMART; SM00410; IG_11ke; 1.
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117 Aa; 12635 MW; E2141AF47115EE78 CRC64;
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117 117
117 AA, 12611 MW, B7BEC87E579CB678 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                 01-077-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
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117 AA
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STRAIN-BROWN NORWAY; TISSUE-TESTIS;
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                                                                                                   C-kit receptor (Fragment).
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Best Local Similarity 100.0
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PRELIMINARY;
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RESULT 12

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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
Han C.-G., Ohtesubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sabakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
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STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001)
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-0157.H7 / EDL933 / ATCC 700927;
MEDLINE-21074935. PubMed=1120651;
Perna N.T., Plunket G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grobeck E.J., Davis N.W., Lim A., Shoan Y., Miller L.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Melch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 16; Length 146; ilarity 100.0%; Pred. No. 6.3e+02; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AA; 16568 MW; 8E2BB95CF7BC1CED CRC64;
                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Putative PTS enzyme II B component.
YADI OR ECS0131.
Escherichia coli 0157:H7.
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Last annotation update)
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                                                                                                      PRT;
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EMBL, ABO05:189; AAG54433.1; ---
EMBL; AP002550; BAB33556.1; ---
InterPro; IPRO4701; BIIA-man.
Pfam; PF03610; EIIA-man.
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                                                                                                   PRELIMINARY;
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Matches 5; Conserv
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  68
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    64 EILDV
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20504483; PubMed=11016950; Marking S. Pan M., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shrogna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swarzaell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.B., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus furiosus.
Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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STRAIN-VI. / DSM 3638 / ATCC 43587 / JCM 8422;
STRAIN-VI. / DSM 3638 / ATCC 43587 / JCM 8422;
The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AEO10189; AAL80810.1;
Hypothetical protein; Complete proteome.
SEQUENCE 139 AA; 16222 MW; 0879C8B7133FCE1A CRC64;
                                                                                                                                                                                                                                                                                        Halobacterium sp. (atrain NRC-1).
Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 119 AA; 13648 MW; 585905ABA983B9B1 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                             119 AA
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Matches 5; Conservative
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                                         109 EILDV 113
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P. Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P., G. C.P., "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
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                                                                                                                                                                                                                                                                                                                                                                                                          Strauberg R.;
Strauberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023062; AAH23062.1; -.
Hypothetical protein.
SEOUENCE 159 AA; 18896 MW; 349F26D187132A15 CRC64;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL, ALS90445; CAD26668.1; -.
Hypothetical protein.
SEQUENCE 163 AA; 18931 MW; 3A36178CB48421FF CRC64;
                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 18-9 kPa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECUO5_1480.
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Pred. No. 6.9e+02;
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Best Local Similarity 100.0
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Encephalitozoon cuniculi.
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les 5; Conserv
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alband D., Eisen J.A., Haft D., Hickey E.,
Reloray J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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MEDLINE=9829987; PubMed=9634230;

Gold S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Gliver S., Geeger K., Skelton S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Deciphering the biology of Mycobacterium tuberculosis from the

Complete genome sequence.";
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"Whole genome comparison of Mycobacterium tuberculosis clinical and
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022004; CAA17660.1; -.
EMBL; AE006976; AAK45118.1; -.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MRA-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv0854.
Rv0854 OR Mrv043.47 OR Mr0877.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

Cronin A., Davis P., Davies R.M., Dowd L., White N., Parrar J.,

Reltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

Reltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

A Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitehead S., Barrell B.G.,

"Complete genome sequence of a multiple drug resistant Salmonella

"In nature 413:848-852(2001).

REMBL; AL627267; CAD05018.1; -.

REMBL; AL627267; CAD05018.1; -.

REMBL; AL627267; All Carboxyl.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriacese;
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MEDILNB=20223866; PubMed=10759889;
Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
Hiraoka Y.;
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                               Length 169;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phosphoribosylaminoimidazole carboxylase catalytic subunit.
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Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales
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   100.0%; Score 23; DB 16; Conservative 0: Mismatch.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
Hypothetical nuclear protein (Fragment).
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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TIGRFAMB; TIGR01162; purE; 1.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phosphoribosylaminoimidazole carboxylase = AIR carboxylase, catalytic subunit (EC 4.1.1.21).
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STRAINELT2 / SGSC1412 / ATCC 700720;

STRAINELT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; Pubmed-11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Buryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
Methanopyrus.
NCBI_TaxID=2320;
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STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Slesarev A.I., Mezhevaya K.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
EMBL; AR010311; AM01336.1; -
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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164 AA; 19130 MW; 02861FCDE99CB69D CRC64;
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                                                                                                                                                                                                                                    Created)
Last sequence update)
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UBIC OR MKO119.
Methanopyrus kandleri.
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InterPro, 1PR0000031; AIR_carboxyl.
Pfam, PF00731; AIRC; 1.
TIGRFAMs; TIGR01162; purE; 1.
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SEQUENCE 169 AA; 17794
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SEQUENCE 164 AP
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                               27 EILDV 31
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Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
Dacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).

EMBL; AB007683; AAK79705.1; -.
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100.0%; Pred. No. 7.5e+02;
tive 0; Mismatches 0;
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Conservative 0
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Matches
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Q8ZC15
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Matches
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   "Large-scale screening of intracellular protein localization in living fisation yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).
EMBL; AB027955; BAA87259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota; Neoptera, Endopterygota; Diptera; Brachycera, Muscomorpha,
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shevelyov Y.Y., Kalmykova A.I.; "Stellate orphon provides a poly(A) signal for bendless mRNA."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 3; Length 171; 100.0%; Pred. No. 7.3e+02; Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.4e+02;
....marches 0; Indels
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FlyBase; FBGN0044817; Stel.2DOR.
FlyBase; FBGN0044817; Stel.2DOR.
Pfam; PF01214; CK II beta; 1.
PRINTS; PR00472; CASKINASEII.
PROSITE; PS01101; CK2 BETA; 1.
SEQUENCE 172 AA; 19525 MW; A2C8752F3A976FBB CRC64;
                                                                                                                                                                                                                       171 AA; 21395 MW; 30012B18345508BE CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Uncharacterized conserved protein (coiled-coil).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 172 AA
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Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                              Local Similarity 100.
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Best Local Similarity
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                                                                                                                             Nuclear protein.
NON_TER 171
NON_TER 171
SEQUENCE 171 AA
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NCBI_TaxID=7227;
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Q9NIV2
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Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
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                                                                                                                                                                                                                                           Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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PROSITE; PSO1128; SHIKIMATE KINASE; UNKNOWN_1.
Kinase; Transferase; Complete proteome.
SEQUENCE 174 AA; 18864 MW; 8D9A1E8BF88730D6 CRC64;
QBZC15 PRELIMINARY; PRT; 174 AA.
QBZC15;
QBZC15;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-UNA-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Shikimate_kinase II (BC 2.7.1.71).
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Last annotation update)
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ilarity 100.0%; Pred. No. 7.5e+02;
Conservative 0; Mismatches 0;
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InterPro; IPR000623; Shik kinase.
Pfam; PF01202; SKI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=CO-92 / BIOVAR ORIENTALIS;
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Wernegreen J.J., Riley M.A.; "Comparison of symbiotic and housekeeping "Comparison of the evolutionary dynamics of symbiotic and housekeeping loci: a case for the genetic coherence of rhizobial lineages."; mol. Biol. Evol. 16:98-113(1999).
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Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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Streptococcaceae; Streptococcus.
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SEQUENCE 180 AA; 20399 MW; 3898616FB9EEF6E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
10.DEC-2001 (TrEMBLrel. 19, Last annotation update)
179pothetical protein SP1280.
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Last annotation update)
                                                                                                                                                                                 Score 23; DB 2; Pred. No. 7.7e+02;
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Pred. No. 7.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                   180 AA
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seque
01-JUN-2002 (TrEMBLrel. 21, Last annot
DNA-directed RNA polymerase subunit E'
RPOEI OR MK1451.
                                                                     EMBL; AF063458; AAD11328.1; -.
InterPro; IPR002509; Polysac_deacet.
Pfam; PF01522; Polysac_deacet; 1.
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                 100.0%;
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ilarity 100.0%;
Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 293:498-506(2001).
EMBL; AE007427; AAK75384.1;
                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
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                                                                                                     Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Matale D.A., Rogozin I.B., Tatuskin K.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin B.V., Kozyawkin S.A., "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";

EMBI, AR010445; AAM02768.1; -. 99:4644-4649(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium sp. WSM870.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                           Length 175;
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                                                                                                                                                                                                                                                                                                                                             Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minick P., Vickerman M.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 1012643; AAG32547.1; -.
Hypothetical protein
SEQUENCE 176 AA; 19929 MW; B73E430114725CFF CRC64;
                                                                                                                                                                                                                                                   Complete protecome.
SEQUENCE 175 Aa; 19325 MW; 695D9BAFFD1AC73B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Nodulation protein B (Fragment).
                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB'17;
100.0%; Pred. No. 7.5e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 176 AA.
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MEDLINE=99261640; Pubmed=10331255;
                                                                   STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcaceae; Streptococcus.
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Beet Local Similarity 100.00
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                  MCBI_TaxID=2320;
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Methanopyrus
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RESULT 27
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Gaps

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Matches

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                    "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.",
                                                                                                                                                Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 17; Length 194;
Pred. No. 8.3e+02;
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Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Mannhaupt
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
EMBL, AE009904; AAL64578.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 194 AA; 21893 MW; 558DA7CC8AA4BF31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22842 MW; 637CDFD14AEA7B16 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 22.8 kba protein.
14C9.40 OR AT4G12200.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 AA.
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                                                 [1]
SEQUENCE FROM N.A.
CHARLE / ATCC 51768 / DSM 7523;
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EMBL; AL161533; CAR7863.1; ...
InterPro; IPR0010978; Znf CCHC. Pfam; PP000098; Zf-CCHC; I. Hypothetical protein. The SEQUENCE 200 AA; 22842 MW; 6
  Thermoproteaceae; Pyrobaculum.
NCBI_raxID=13773;
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                              Slearev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.; Wolf Y.I., Stetter K.O., "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens."; Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).

EMBL, AR010437; AAM02664.1; -- DNA-directed RNA polymerase; Complete proteome. SEQUENCE 183 AA; 20754 MW; C43AA6784B63750D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
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Last sequence update)
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequenc
01-UUN-2002 (TrEMBLrel. 21, Last annotat
Fibronectin variable region (Fragment).
Bos taurus (Bovine).
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                                                                   STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
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EMBL; AF260305; AAF91381.1; -.
InterPro, IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
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NCBI_TaxID=2320;
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56 EILDV
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Q9MZ31
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082U30
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Debelle F., Plazanet C., Roche P., Pujol C., Savagnac A.,
Rosenberg C., Prome J.C., Denarie J.;
Rosenberg C., Prome J.C., Denarie J.;
Fine NodA protechins of Rhizobium meliloti and Rhizobium tropici specify
the N-acylation of Nod factors by different fatty acids.";
Mol. Microbiol. 22:303-314(1996).
EMBL, X98514; CAA67138.1; -.
EMBL, X98514; CAA67138.1; -.
EMBL, POLYSEC, POLYSEC deacet.
Plan, PPOLS22; Polysec deacet.
Fran, PRO1522; Polysec deacet.
SEQUENCE 219 AA; 23566 MW; 7394719AFFB1743C CRC64;
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MEDLINE-99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.C., Ketchum K.A.,
Haft D.H., Hickey B.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Vonter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
EMBL, AR001708, AAD35348.1; -.
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Gaps
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=398;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein TM0260.
                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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 Mismatches
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Pfam; PF01865; DUF47; 1.
Hypothetical protein; Complete proteome.
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38 BILDV 42
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Q53253
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Q9WY98
 Matches
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                                                                                                                                                                                                                                                                                                                     Kullman S.W., Matsumura F.;

"Identification of a novel cytochrome P-450 gene from the white rot fundauge Phanerochaete chrysosporium.";

-1- SIMILABITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL; AF005475; AAB63277.1; -.

InterPro; IPR001128; Cytochrome_P450.

PRINYS; PR00385; P450.

PRNNYS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                             Eukaryota, Pungi, Basidiomycota, Hymenomycetes, Homobasidiomycetes, Aphyllophorales, Corticiaceae, Phanerochaete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Godfrey H.P., Ebrahim A.A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBU databases.
EMBL, "141850; ADMO0014.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
23232 MW; B3741B219D6pB631 CRC64;
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Pred. No. 9e+02;
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SEQÜENCE 208 AA; 24096 MW; 8254CI
                                                                                        Created)
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InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
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MEDLINE=97355939; PubMed=9212420;
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                                                                                                                                          Cytochrome P450 (Fragment).
CYP63-1A.
Phanerochaete chrysosporium.
                                                                                                                       (TrEMBLrel. 20,
                                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05,
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                                                    PRELIMINARY;
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212 AA;
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Best Local Similarity
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RESULT 35 095609

Matches

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"The genome of the natural genetic engineer Agrobacterium tumefaciens 5.8\, ",
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                                                                                                                                                                                                                                                                                                                                           EMBL; AE009279; AAL44307.1; -. EMBL; AE008333; AAK89900.1; -.
                                                                                                                                                                                                                                                                                                                            Science 294:2323-2328(2001).
                                                            Science 294:2317-2323(2001).
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity 100.vv
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SEQUENCE 242 AA
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"Autoinduction regulates production of novel antifungal metabolites in Pseudomonas fluorescens BLo15.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF232768; AAF61718.1;
InterPro; IPR001690; Autoind synth.
Pfam; PF00765; Autoind synth; 1.
PRINTS; PR01549; Autoind synth; 1.
PROSTE; PS00949; AUTOINDUCERS_SYNTH; 1.
PROSITE; PS00949; AUTOINDUCERS_SYNTH; 1.
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almada N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphinmachak C., Wu Z., Romero P., Gordon D.,
Zhang G., Yoo H., Tao Y., Bille P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.V.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                    Gaps
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
101-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypochetical protein Atu4994.
ATU3494 OR AGR L. 2665.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                     100.0%; Score 23; DB 16; Length 222; 100.0%; Pred. No. 9.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 226;
                                                                                  0; Indels
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222 AA; 25926 MW; 22E680FFB3CB3B52 CRC64;
                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative acylhomoserine lactone synthase.
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100.0%; Pred. No. 9.5e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                               226 AA
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                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                         Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas fluorescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas.
NCBI_TaxID=294;
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                                                                                                                                                                    95
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                                                                                                                          1 EILDV 5
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                                                                                                                                                                91 EILDV
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SEQUENCE
                                        Query Match
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                                                                                                                                                                                                                                   RESULT 38
Q91606
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SECUENCE FROM N.A.
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Glelo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X STRAIN=DELTA H;

X MEDLINE=98037514; PubMed=9371463;

X MEDLINE=98037514; PubMed=9371463;

A Gmith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,

A Adredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum

T deltaH: functional analysis and comparative genomics.";

L J. Bacteriol. 179:7135-7135-115.

EMBL; AE000887; AAB85681.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 231;
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Methanobacteriaceae; Methanothermobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 231 AA; 25246 MW; 59110EA68CE538AB CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 AA.
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MEDLINE=98065943; PubMed=9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Felstchmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artlach P., Bowman C.,
Garland S., Fuji C., Cotton M.D., Horet K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxcon M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 16; Length 253; ilarity 100.0%; Pred. No. 1.1e+03; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic sequence of a Lyme disease spirochaete, Borrelia
             Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003743; DUF164.
Pfam; PF02591; DUF164; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 29838 MW; 20169A5790F824E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetacese, Borrelia.
                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
BHypothetical protein BB0713.
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             Mismatches
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MEDLINE=94150718; Pubmed=7906398;
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01-JUN-1998 (TrEMBLrel. 06, Ls
01-DEC-2001 (TrEMBLrel. 19, Ls
H10D12.2 protein.
H10D12.2.
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EMBL; AE001171; AAC67060.1;
TIGR; BB0713; -.
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               Conservative
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Matches 5; Conserv
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051655
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SEQUENCE FROM N.A.

SEQUENCE FIRST / RIMD 0509952;

MEDIINES-1156231; PubMed=11258796;

MEDIINES-1156231; PubMed=11258796;

A Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

R.Onsplete genome sequence of enterchemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

I. DNA Res. 8: 11-22(201);

I. BMBL; ARG0376-1;

R. EMBL; ARG035457; AAG57376.1;

R. REMBL; ARG03281; HQCH_HpaI.

R. RIMCHPRO; IPRO05000; HQCH_HpaI.

P. Fami, PF03128; HQCH_HpaI.

W. COMPLETE FOLCEOME.

SEQUENCE 250 AA; 26948 MW; 423FFFC817975600 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Agctbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anancharama T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orf, hypothetical protein.
23503 OR ECS3130.
Escherichia coll 0157:H7.
Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                       Grimaldi C., Dutertre M., Simonet J.M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR138861; ARG1982.1;
Hypothetical protein:
SEQUENCE 246 AA; 28789 MW; EA82CCE2178252AF CRC64;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Myochelical 28.8 kDa protein.
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STRAIN=ATCC 35092 / DSM 1617 / P2;
STRAIN=ATCC 35092 / DSM 1617 / P2;
STRAIN=21312956; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantãe, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Cicereae, Cicer. NCBI_TaxID=3827;
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Verma P.K., Kumar V., Singh P.K., Upadhyaya K.C.;
"Isolation of a cDNA clone encoding a putative Hs1pro-1 homolog from
                                                                                                                                                                                                           Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 23; DB 17; Length 267; 3est Local Similarity 100.0%; Pred. No. 1.1e+03; 4atches 5; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chickpea.";
Submirted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ATO 20680; AAK72104.1; -
SEQUENCE 268 AA; 30773 MW; A91E326F80E108CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 AA; 29663 MW; F485C1E07E92674A CRC64;
                                                                                       01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTUN-2002 (TrEMBLrel. 21, Last annotation update)
Exthrocyte band 7 membrane protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putalive Hsipro-1-like protein.
Cicer arietinum (Chickpea) (Garbanzo).
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PRINTS; PR00721; STÖMATIN.
SMART; SM0244; PHB; 1.
Complete; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 267 AA; 29663 MW; F485C1E07E92674A CR.
                                                                   267 AA.
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                                                                   PRT;
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INTERPRO; IPR001107; Band 7.
INTERPRO; IPR001972; Stomatin.
INTERPRO; IPR000531; TonB boxC.
                                                                   PRELIMINARY;
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Q97WL9
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Parsons J., Percy C., Rifken D., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1021;

MEDLINE=21365609; PubMed=11481432;

Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Barnot-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

'"Nucleotide sequence and predicted functions of the entire

Sinorhizoblum melliolty BymA megaplasmid.";

Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTC-2002 (TrEMBLrel. 19, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Nitrate transport ATP binding protein, probable.
RA0305 OR SMA0581.
RAizobium meliloti (Sinorhizobium meliloti).
Plasmid psymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 5; Length 25
100.0%; Pred. No. 1.1e+03;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                     Ozersky P.,
"The sequence of C. elegans cosmid H10D12.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038620; AAB93487.1; -.
SEQUENCE 256 AA; 28085 WW; B93E1E6AFA44CD3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29691 MW; D04197F9A515D605 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00211; ABC TRANSPORTER; UNKNOWN_1. Plasmid; Complete profeome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003439; ABC_transportr. Pfam; PF00005, ABC tran; 1. Pr00000m; PD0000006; ĀBC_transportr; 1. TIGRPAMS; TIGR01184; ntrCD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 AA;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=BRISTOL NZ;
                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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75 EILDV 79
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STRAIN-BROWN NORWAY; IISSUB-TESTIS; Gangadharan S., Ali S.; Gangadharan S., Ali S.; Gangadharan S., Ali S.; Gangadharan S., Ali S.; Gangadharan S., Ali S.; Submitted MRNA transcript of c-kit (encompassing extracellular domain) originating from testis of 1 day old rat."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. BMBL; AR296694, AR468585.1; -... InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                     01-47-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 17, Last annotation update)
01-UUN 2001 (TrEMBLrel. 17, Last annotation update)
C-kit receptor (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to DnaJ (Hsp40) homolog, subfamily B, member 10.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC011090; AAH11090.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER 274 274 SEQÜENCE 274 AM; 000FA042B09D0103 CRC64;
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277 Aa; 30675 MW; 6D9198A5C4FA1DA3 CRC64;
                                                                                                                                                                                                                                274 AA
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                                                                                                                                                                                                                                PRT;
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InterPro; IPR002950; Josephin.
InterPro; IPR003903; UIM.
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nes 5; Conservative
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Pfam; PF02809; UIM; 2.
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                                            251 EILDV 255
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69 EILDV 73
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0921S2
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"Genetic analysis of a chromosomal region containing vanA and vanB, genes required for conversion of either ferulate or vanillate to protocatechuate in Acinetobacter.";
J. Bacteriol. 181:3494-3504(1999).
-i- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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InterPro; IPR000285; HTH_ICIR.
Pfam, PF01614; ICIR.
SMART; SM00346; HTL, ICIR.; 1.
DNA-binding; Hypotherical protein; Transcription regulation.
SEQUENCE 270 AA; 30524 MW; DB457B57BF817FBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Acinetobacter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 2; Length 270; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches, 0; Indel8
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100.0%; Score 23; DB 4; Length 271;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 5; Conservative 0; Mismatches' 0; Indels
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InterPro; IRRO1A918; Znf CCHC. Pfam; PRO0098; zf-CCHC, 4.
Pypochetical protein. Submar: School Protein. SEQUENCE 271 AA; 30477 MW; D68EDABE8B9D0F3D CRC64;
                                                                                                                                                                                                                                                        024845;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 30.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 30.5 kDa protein.
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                                                                                                                                                                                                                                270 AA
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Homo sapiens (Human).
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TISSUE=AMYGDALA;
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                                                       156 EILDV 160
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| S0 EILDV 54
1 EILDV 5
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Best Local Similarity
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STRAIN-CZA / ATCC 35395 / DSM 2834;
MRDLINE=1192760; PubMed=1193238;
Galagan J.E., Nusbaum C., Ferdrizzi M.G., Macdonald P.,
FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
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Ohta S., Yohda M., Ishizuka M., Hirata H., Hamamoto T.,
Otawara-Hamamoto Y., Matsuda K., Kagawa Y.;
"Sequence and over-expression of subunits of adenosine triphosphate synthase in thermophilic bacterium PS3.",
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Kagawa Y., Ishizuka M., Saishu T., Nakao S.;
"Stable structure of thermophilic proton ATPase beta subunit.";
J. Blochem. 100:923-934(1986).
EMBL; X07804; CAA30654.1; -..
EMBL; X04609; CAA28276.1; -..
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NCBI_TaxID=2334;
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TIGREPMs; TIGRO1146; ATPBYD. Frgamma; 1.
PROSTIE; PSO0153; ATPASE GAMMA; 1.
SEQUENCE 282 AA; 31778 WW; PAITCE9482EEE9F7 CRC64;
                                                                                                                                                                                                        OS2412; O56245; O52409; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
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Last sequence update)
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01-JUN-2002 (TrEMBLrel. 21,
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EILDV 10
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Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B., "The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                    Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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Pasteurella.
                                                                                                                                                                                                                                                                      Length 285;
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                                                                                                                      and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL, AE011086; AAM07103.1; -.
COMPLETE profesome.
SEQUENCE 285 AA; 32209 MW; 9AEBDB37DA8868F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein PM0569.
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Last sequence update)
Last annotation update)
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MEDLINE=21145866; Pubmed=11248100;
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SECURNCE FROM N.A.

STRAIN=MCS8 / SEROGROUP B;

STRAIN=MCS8 / SEROGROUP B;

MEDLINE=2017575; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.B.,

Bisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey B.K.,

Haft D.H., Salzberg S.L., White O., Pelschmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parkes D.S., Blair B., Cittone H., Clark B.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

McComplete genome sequence of Neisseria meningitidis serogroup B strain
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Richherford K.M., Simonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.", Naturel 404:502-506(2000).

EMBL; All62755; CAB84611.1; -. InterPro; IRR002500; PARS reduct.
Fransferse; Nucleotidyltransferase; Complete proteome. SEQUENCE 307 AA; 34724 MM; 6D2AlE060G31124C CRC64;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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Pfam; PF01507; PAPS reducf., 1.
Transferase; Nucleotidyltransferase; Complete proteome.
SEQUENCE 307 AA, 34696 MM; 4BFP5DB3861D0FD3 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
Sulfate adenylyltransferase, subunit 2.
NMB1192 AND NMB1154.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
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llarity 100.0%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 0;
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Best Local Similarity
The 5; Conserve
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Q9JS34
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2000 (TrEMBLrel. 19, Last sequence update)
01-0cr-2001 (TrEMBLrel. 19, Last annotation update)
Putative sulphate adenylate transferase subunit 2 (EC 2.7.7.4).
CYSD OR NMALS 55.
Nelsseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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Pubmed=11842084;
Pubmed=11842084;
Jones P.A., Samuels N.M., Phillips N.J., Munson R.S. Jr., Bozue J.A., Arseneau J.A., Nichols W.A., Zaleski A., Gibson B.W., Apicella M.A.; "Haemophilus influenzae Type b Strain A2 Has Multiple Sialyltransferases Involved in Lipooligosaccharide Sialylation."; J. Biol. Chem. 277:14588-114611(2002).

EMBL; AY061634; AAL38659.1; 49645B7931FFBDF90 CRC64; SEQUENCE 304 AA; 36115 MW; 49645B7931FFBDF90 CRC64;
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STRAIR=2191, SENCHYPE 4A;
MEDLINE=2291, SENCHYPE 4A;
MEDLINE=2292556; PubMed=10761919;
Parkhill J., Achtuan M., James K.D., Bentley S.D., Churcher C.,
Rlee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
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Haemophilus.
             "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
EMBL; 281509, CAB64157.1; -.
Interpro; IPR003582; BAF-11ke.
Interpro; IPR003582; ShKT.
SMART; SM00181; EGF; 1.
FROSTIE; PS000221; EGF 1; UNKNOWN 1.
SEQUENCE 290 AA; 32686 MW; 700F9BBE116FEADT
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Q0RLZ4
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DD Q0RLZ2
DT O1-JU
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09500
AC 09500
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SECUENCE FROM N.A.
TISSUE-BRAIN PARIETAL LOBE;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.,
"Isolation of full-length cDNA clones from macaque brain cDNA
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to protein phosphatase 2, regulatory subunit B (B56), beta isoform (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 35.5 kDa protein.
Macaca faccicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Coiled coil; Hypothetical protein; Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 6; Length 317; ilarity 100.0%; Pred. No. 1.3e+03; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047624; BAB12148.1; -.
HSSP; PS6536; 2KIN.
                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Motor protein.
SEQUENCE 317 Aa; 35489 MW; 28FDC60C4F75A684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 AA; 36619 MW; BF6F70007B3E9081 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 23; DB 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 5; Conserv
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                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 EILDV 78
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SEQUENCE
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Q97PP0;
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Q97PP0
ID Q97PP1
AC Q97PP1
DT 01-OC
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Hilbert H., Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, A0131907; CAA21428.1; -.
InterPro; IPR0011813; 608 ribosomal.
InterPro; IPR001790; Ribosomal L10.
Pfam; PF00428; 608 ribosomal; 1.
Pfam; PF00466; Libosomal L10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                             Vibrio parahaemolyticus.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 23; DB 2; Length 30 Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   McCarter L.L.;
"Polar Flagellar Region I.";
Submitted (ARP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, U12817, AAD42910.1; -.
HSSP; P06143; IABG.
InterPro; IPR002545; CheW.
InterPro; IPR00189; Response_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNOV-2001 (TrEMBLrel. 17, Last annotation update)
SPCT8 14C.
SPCT8 1.4C.
SChizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes;
Schizosaccharomyces.
Schizosaccharomyces.
NOBI TAXID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pram; Pro1584; CheW; 1.
Pram; Pro1072; response_reg; 1.
ProDom; PD000039; Response_reg; 1.
SMART; SM00260; CheW; 1.
SMART; SM0048; REC; 1.
Phosphorylation; Sensory transduction.
SEQUENCE 308 AA; 34126 MW; 5E21A365839BB978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribosomal protein.
SEQUENCE 312 AA; 33565 MW; 68979A46B921F761 CRC64;
         01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                          NCBI_TaxID=670;
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145 EILDV 149
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SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MIDLINE=21311952; PubMed=11418146;
MIDLINE=21311952; PubMed=11418146;
MIDLINE=21311952; PubMed=11418146;
MIDLINE=111952; PubMed=11418146;
MIDLINE=111952; PubMed=1141814, Magai Y., Lian J.-O., Ito T.,
MIDLINE A., Matsumaru H., Maruyama A., Maruyama A., Maruyama H., Mattori M., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kannehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba Thattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                       Bacteria, Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23, DB 16; Length 321; 100.0%; Pred. No. 1.3e+03;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Pyridine nucleotide-disulphide oxidoreductase family
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNA-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein SAV0553.
SAV0553 OR SA0511.
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InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001013; PyrIdine_redox_2.
InterPro; IPR001100; Pyr_redox.
Pfam, PF00070; pyr_redox; I.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00469; PADPNR.
PRINTS; PR00461; PNDRDTASEI.
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21357209; PubMed=11463916;
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EMBL; AE007451; AAK75650.1; -.
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NCBI_TaxID=158878, 158879;
                                                                                                                                                          Streptococcus pneumoniae.
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Nature 417:141-147 (2002).

-!- FUNCTION: THE SIGNA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY. ECF SUBFAMILY.

EMBL, AL109962; CAB53126.1;
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"A set of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicalor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                       Gaps
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STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challie G.L.,

Homson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Tarper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,

Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                             Length 321;
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   Indels
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00776; Sigma70 ECF; I.
DNA-binding; DNA-directed RNA polymerase; Sigma factor;
aureus.";
Lancet 357:1225-1240(2001).
EMBL; AP003359; BAB56715.1; -.
EMBL; AP003130, BAB41742.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 321 AA; 36053 MW; E0B08B19CF630CB0 CRC64;
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SEQUENCE 322 AA; 35466 MW; C4EE8BA53849677D CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                      100.0%; Score 23; DB 16;
ilarity 100.0%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 0;
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"The complete genome sequence of the gastric pathogen Helicobacter \mathrm{pylori.}\,,
                                                                                      Nature 388:539-547(1997).
EMBL; AE000622; AAD08209.1;
TIGR; HP1164; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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4 EILDV 8
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         Venter J.C.;
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Q92K51;
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STRAIN=26695 / ATCC 700392;
MEDLINE=9739467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                            Gaps
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HP1164.

HP1165.

HP11cobacter pylori (Campylobacter pylori).

Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;

Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                           100.0%; Score 23; DB 16; Length 322; 100.0%; Pred. No. 1.3e+03; ive 0; Mismatches 0; Indels
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011609; AAH11609.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00636; DNAJ 1; UNKNOWN 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS00294; PRENTLATION; UNKNOWN 1.
SEQUENCE 324 AA; 35580 MW; 0154ED3E29F34B4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Dnad (Rep40) howolog, subfamily B, member 2.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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100.0%; Pred. No. 1.3e+03;
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InterPro; IPR002950; Josephin.
InterPro; IPR00393; Prenyl_site.
InterPro; IPR003903; UIM.
Pfam; PF00226; DnaJ; 1.
Pfam; PF02809; UIM; 2.
Query Match
Beet Local Similarity 100.v.
E.hem 5; Conservative
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                                                                                                                                                                                               148 EILDV 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative thioredoxin reductase.
TXRB 2 OR UHP1011.
Helicobacter pylori 999 (Campylobacter pylori 199).
Bacteria, Proteobacteria, epsilon subdivision, Helicobacter group;
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100.0%; Score 23; DB 16; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastric pathogen Helicobacter pylori.";

Nature 397:176-180(1999).

L. COPACTOR: FAD (1999).

EMBL, ABON1536, AAD06662.1;

InterPro; IPR001759; Adrndx_reductase.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

PRINTS; PR00419; ADRDTASE.

PRINTS; PR00419; ADRDTASE.

PRINTS; PR00469; PNDRDTASEI.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

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PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.
                                                                                                                                                                                                                                                                      Indels
TICN, TETPLO, 1PR001327, FAD_pyr_redox.

Pfam; PF00070; pyr redox; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 324 AA; 35986 MW; 0854598651D92B30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                              100.0%; Score 23; DB 16;
ilarity 100.0%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 0;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
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STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINB-20570466; PubWed=11121031;
Kawashima T., Amano N., Kolke H., Makino S.-I., Higuchi S.,
Kawashima T., Yamanouro K., Yamazaki M., Kanehori K., Kawamoto T.,
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S. 497:14257-14262 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21595265; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Kishida Y., Kohara M., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing cyanopacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 23; DB 16; Length 337; Best Local Similarity 100.0%; Pred. No. 1.4e+03; Matches 5; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaeā; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                  Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
      IndelB
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EMBL; AP003588; BAB73886.1; -.
Hypothetical protein; Complete proteome

SEQUENCE 337 AA; 39125 MW; 9E6A546CPEFBF6BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
Phosphoribosylfcraylglycinamide cyclo-ligase.
TV0165 0R TVG0175535.
                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Alr2187.
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    Mismatches
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InterPro; IPR004733; PurM_cligase.
Pfam; PF00586; AIRS; 1.
TIGRPAMs; TIGR00878; purM; 1.
Ligase; Complete proteome.
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    5; Conservative
                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                    RESULT 71
Q8YUZ4
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Q97CD7
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                                                                                                                                                                                      MEDLINE-98049343; PubMed-9389475; Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Doupherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Watdman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Pujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Mature 390:364-370(1997).
EMBL, AE000986, AAB89555.1; --
HSSP, PO8178; ICLI.
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MEDLINE=20500219; PubMed=11048724;
Glass JG.H. Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
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Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
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Pfam; PF00566; AIRS C; 1.
TIGRFAMS; TIGR00878; purM; 1.
Hypothetical protein; Ligase; Complete proteome.
SEQUENCE 329 AA; 36209 MW; C9D291148AE3DD34 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Phosphoribosylformylglycinamidine cyclo-ligase (PURM).
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                                                                                   Archaea; Buryarchaeota, Archaeoglobi, Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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100.0%; Pred. No. 1.3e+03;
iive 0; Mismatches 0;
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EMBL; AE002107; AAF30482.1; -.
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100.0%;
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Best Local Similarity luv...
5; Conservative
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                                                               Archaeoglobus fulgidus.
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Q9PR68; **09PR68**

99 PR 68 PP 11 D PP 68 PP 12 PP 12 PP 13 PP 14 PP 14 PP 15 P

RESULT 70

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Query Match 100.0%; Score 23; DB 2; Length 344; Best Local Similarity 100.0%; Pred. No. 1.4e+03; Matches 5; Conservative 0; Mismatches 0; Indels ...
                                                                                                                                                                   344 AA; 39018 MW; 07B0353EC7F43FFD CRC64;
InterPro; IPR000090; Flg_Motor_Flig.
Pfam; PF01706; FligG-C; 1.
PRINTS; PR00954; FLGMOTORFLIG.
TIGRPAMB; TIGR00207; flig; 1.
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                                                                                                                                 Flagella.
SEQUENCE
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Ge Y., Old I., Saint Girons I., Yelton D.B., Charon N.W.;
"Filth and fill of Borrelia burgdorferi are similar to flagellar and
virulence factor export proteins of other bacteria.";
Gene 168:73-75(1996).
EMBL: L76303, AAB51411.1; -.
EMBL: U79711; AAB41945.1; -.
HSSP; Q9Wf61; 10C7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              093HG3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last sequence update)
01-JWA-2002 (TrEMBLrel. 21, Last annotation update)
3-oxoacyl-(acyl carrier protein) synthase III.
Bacteptomyces avermitilis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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                                                                100.0%; Score 23; DB 17; Length 338; 100.0%; Pred. No. 1.4e+03;
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
   338 AA; 37183 MW; 0AC488696971DEF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA.
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                                                                                                                                    0, Mismatches
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   SEQUENCE
                                                                    Query Match
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(934G3
D) 0934G3
D) 0934G
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MEDLINE=21624277; PubMed=11752168;
Afonso C.L., Tulman B.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
Kutish G.F., Rock D.L.;
"The genome of swinepox virus.";
J. Virol. 76:783-790(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Afonso C.L., Tulman B.R., Lu Z., Balinsky C., Osorio F.A., Zsak L., Kutish G.F., Rock D.L.;
Submitted (AuG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF410153; AAL69867.1; -.
InterPro; IPR002225; 3Beta HSD.
InterPro; IPR00977; DNA 11gase.
Pfam, PF01073; 3Beta HSD.
PROSITE; PS00697; DNA LIGASE A1; UNKNOWN 1.
SEQUENCE 344 AA; 39342 MW; ECD28807FEDE018 CRC64;
                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Suipoxvirus.
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                                                01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
sPV128 hydroxysteroid dehydrogenase-like protein.
  344 AA.
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PRT;
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Best Local Similarity 100.v.,
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Peptide #3 recogni Fibronectin CS1-de Fibronectin CS1-de

Scoring table:

Searched:

Minimum DB Maximum DB

Database

score:

Title: Perfect

Sequence:

protein

Run on:

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AAX77444
AAX77444
AAR11361
AAR2888
AAR41369
AAR92536
AAW25130
AAW25130
AAW313862
AAW313862
AAW313862
AAW313862
AAX32862
AAX32862
AAX32862
AAX32862
AAX32863
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Cell adhesion pept
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                                                                   Search time 35 Seconds
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19.036 Million cell updates/sec
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          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                    908470 segs, 133250620 residues
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Maximum Match 100%
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AAW25192
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Alpha 4Beta 1 interest of peptide fragm Peptide portion especial peptide portion especial peptide portion especial peptide portion especial peptide sequent integrin-binding peptide sequent integrin-binding peptide sequent integrin-binding peptide sequent peptide sequent peptide sequent integrin-binding peptide sequent integrin-binding peptide sequent integrin-binding peptide sequent integrin-binding peptide sequent integrin-binding peptide sequent integrine inte

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Score

Result ŝ 1064597890

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AAW33337 AAW31690 AAX32863 AAX32875 AAW8067 AAW81844 AAX77410 AAX77410 AAX77410 AAX77410 AAX3690 AAX13416 AAX43416 AAX49890 AAB49890	·	5 AA.		ling inhi	dhesion molecute blood cell; fibronectin; eve site.		Location/Qualifiers 5 /note= "Val-NH2"				÷	CORP.	Vanderslice		LDV domain 1-4, beta-1 i	35pp; English	cule-1 (Nes that list to the state of the st
2325 23 23 23 25 25 25 25 25 25 25 25 25 25 25 25 25		ptide;	entry)	n bind	ill adhesion white blood rry; fibroned		ion/Qu = "Val			271830	271830	NOLOGY	Ren K,		on the alpha n		n mole l cell binds ntigen ite bl adhere e capi migra to the
84 23 100.0 86 23 100.0 87 23 100.0 88 23 100.0 89 23 100.0 90 23 100.0 91 23 100.0 92 23 100.0 94 23 100.0 95 23 100.0 96 23 100.0 97 23 100.0 98 23 100.0 99 23 100.0 99 23 100.0		AAR95719 standard; peptide; AAR95719:	996 (first	Alpha-4Beta-l integrin	VCAM-1; vascular cell adhesion minhibitor; binding; white blood tissue damage; injury; fibronect CS1; CS5; H1; LDV; active site.	Synthetic.	Key Location Modified-site /note=	US5510332-A.	23-APR-1996.	07-JUL-1994; 94US-0271830	07-JUL-1994; 94US-0271830	(TEXA-) TEXAS BIOTECHNOLOGY	Beck PJ, Kogan TP, F	WPI; 1996-221274/22.	New peptide(s) based on inhibiting binding of al fibronectin or invasin	Disclosure; Column 21-22;	Vascular cell adhesion molecule-1 (surface of endothelial cells that l VCAM-1 recognises and binds to the VCAM-1 for very late antigen-4), a surface of certain white blood cells to adhere to the tissue surrounding the capillary hat this white blood cell migration can blood cells flooding to the scene, Cpds. capable of blocking this proc

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agents. IA4B1 also recognises the extracellular matrix glycoprotein fibronectin. Three distinct IA4B1-binding sites have been identified within fibronectin. One site is found in the Heplir region and is expressed in all isoforms; two others (CS1 and CS5) are present in the alternatively spliced type III connecting segments. CS1 has the higher affinity for IA4B1 and contains the tripeptide LDV as its minimal active site. Peptides AAR95704-805 are modeled after a portion of the CS1 peptide that include the LDV domain presented in such a way by its novel flanking sequence to produce a potent inhibitor of IA4B1 binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW25187-W25192 are peptides containing an LDV sequence or equivalent. The peptides are capable of binding to cell adhesion molecules and are used in aqueous irrigation solutions for use during and after endoscopic operations. Preferred irrigation solutions are necessistic or more electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV and/or KEDV (given in one letter amino acid code). The solutions are especially used for irrigating the bladder during and after tumour removal by transurethral resection. The peptides protect against recurrence of tumours.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDV; leucine; aspartic acid; valine; cell adhesion molecule;
binding; bladder irrigation; tumour removal; endoscopic operation;
transurethral resection; cancer; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endoscopic irrigation solns. - contg. peptide(s) that bind to cell adhesion molecules
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                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDV-peptide capable of binding cell adhesion molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                AAW25192 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 8; 8pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FREP ) FRESENIUS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-133793/13.
                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                    5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-1998
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                                                                                                                                                                                                                                                                                                                1 EILDV
                                                                                                                                                                                                                                                                                          1 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW25192;
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                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
AAW25192
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Integrin-ligand; dissociator; disaggregation; platelet thrombus; stroke; fibrinogen; glycoprotein Inb-IIIa; angina; mycastial infarction; bone; osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy; psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                 Disaggregating a ligand:integrin receptor complex
                                                                                                                                  organ transplant rejection; arthritis; ILD
                                                    Integrin ligand dissociator (ILD) peptide.
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10; 39pp; English
                          16-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                  (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-243586/20
                                                                                                                                                                                                                                                                        03-SEP-1997;
                                                                                                                                                                                         WO9911280-A1
                                                                                                                                                                                                                                              03-SEP-1998;
                                                                                                                                                                                                                    11-MAR-1999
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ت
                                                                                                                                                              Synthetic.
 AAY03855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
 The present sequence is a linear stretch of amino acids (present in fibronectin) recognised by the integrin alpha4betal. Integrins are cell surface receptors. The pencon base protein (one of the coat proteins) of adenoviruses binds to integrins. The integrins not only proteins) of adenoviruses binds to integrins. The integrins not only proteins of adenoviruses binds to the extracellular matrix molecules. The mediate cellular adhesion to the extracellular matrix molecules. The acell in vitro having a particular cell surface binding site. The acell in vitro having a particular cell surface binding site. The adenovirus is contacted with a bispecific molecule comprising a component that selectively binds a binding domain of the penton base protein of the adenovirus and a second component that selectively binds the cell surface binding site. A complex of the adenovirus and the bispecific molecule is formed, and the cell is contacted with it to allow entry of the adenovirus into the cell. The methods can be used for research and the
                                                                                                                                                                                                                 penton base protein; coat proteins; adenovirus; binding site; cellular adhesion; extracellular matrix molecule; binding domain; cell surface binding site; bispecific molecule; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods for introducing adenovirus into cells - used for genetic engineering and gene therapy
                                                                                                                                                                                                      surface receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 19;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       뎐,
                                                                                                                                                                                                    Fibrinogen; integrin; alpha-IIb-beta3; cell
                                                                                                                                                                           Peptide recognised by integrin alpha4etal.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kovesdi I, McVey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; Column 2; 56pp; English.
                                                                                            AAW46318 standard; Protein; 5 AA
                                                                                                                                                                                                                                                                                                                                                        96US-0634060.
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                                                                                                                                                (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bruder JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-119984/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            (GENV-) GENVEC INC.
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                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1994;
                                                                                                                                                                                                                                                                       Unidentified
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                                                                                                                                               08-MAY-1998
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                                                                                                                                                                                                                                                                                                                             27-JAN-1998.
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Wickham TJ;
                          1 EILDV
                                                                                                                       AAW46318;
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                                                                 RESULT 3
                                                                                AAW46318
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98WO-US18305.

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The invention relates to integrin ligand dissociators. Disaggregation of an existing platelet thrombus in a blood vessel is due to dissociation of the invention gloopprotein ID-IIIa. This dissociator at ligand binding site I of discoprotein ID-IIIa. The invention provides a method of disaggregating an existing platelet thrombus in a blood vessel, where the platelet comprises thrombus may form an occlusion of a blood vessel, in a subject comprises thrombus may form an occlusion of a blood vessel, in a subject comprises administering a compound which dissociates fibrinogen bound to a first confirmation of a loop of a second contract thrombus. The method is used to treat humans with unstable condition and any caute myocardial infarction. The methods can be cused to enact de-adhesion of osteoloasts from the bone surface to halt be used to enact de-adhesion of osteoloasts from the bone surface to halt condition associated with andiogenesis, e.g. cancer, diabetic retinopathy, psoriasis. Inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. arthritis, inflammatory conditions, e.g. concert, diabetic departure from the current granters granters from the methods can element prior to formation elements in the entermatical elements and intere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents an integrin ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dissociator (ILD) that can be used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 20;
llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5 AA;
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Gaps

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Indels

Conservative

1 EILDV

ò 셤 AAY03855 standard; peptide; 5 AA.

AAY03855 ID AAY0 XX RESULT 4

Chen PG;

Huyghe BG,

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The invention relates to peptidomimetic compounds (AAY77415-Y77438)

Capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CC CA940(7029) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the maturation and trafficking. VLA-4-mediated

CC important role in the maturation and trafficking. VLA-4-mediated

CC important role in the maturation and trafficking. VLA-4-mediated

CC critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory condition, who as as as a stanka, theumatory act to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, ciabetes, inflammatory bowel disease, kidney inflammation and createnosis, prior art inhibition of VLA-4(CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immunoir response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in CC comparison to the CS-1 peptide and therefore lass expensive to comparison to the CS-1 peptide and therefore lass expensive to comparison to the CS-1 peptide to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide for invary 1 to make and is subject to rapid proteolytic comparison to the CS-1 peptide for invary 1 to make and is subject to rapid proteolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1; CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative; arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder; autoimmune disorder; respiratory disorder; LDV motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 21; Length 5; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 243pp; English.
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                                                                                                                                                                                                 98WO-US26605.
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                                                                                                                                                                                                                                                                                                                                                                                               Elices MJ,
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Best Local Similarity الاست
الاستراكة Si Conservative Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disorders
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                                                                   WO200002903-A1
                                                                                                                                                                                                                                                                                                                                  (CYTE-) CYTEL
                                                                                                                                                                                                                                                                                                                                                                                               Arrhenius TS,
                                                                                                                                                                                                 15-DEC-1998;
                                                                                                                                                                                                                                                              10-JUL-1998;
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                                                                                                                                    20-JAN-2000
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      Mammalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       System for reconstructing osseous tissue, useful e.g. for treating fractures, comprises scaffold containing promoter of bone formation and inhibitor of bone resorption -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel system for reconstitution of osseous
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                                                                                                                          Bone regenerative; osteopathic; osseous tissue; reconstitution; scaffold matrix; bone formation promoter; bone resorption inhibitor; cell adhesion; osteoblast; osteoclast; bone defect; fracture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibronectin CS1-derived peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 32; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY77442 standard; peptide; 5 AA
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06-JUN-2000 (first entry)
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                                                             Cell adhesion peptide #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000.
                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Budny JA;
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Sequence

Matches

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Gaps

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The invention relates to a method for treating a mammal with, or at risk of developing, chronic renal failure, involving the administration of at least one integrin antagonist. The integrin antagonists that may be used in the method include antagonists of alpha-1-subunit containing integrins or antagonists of alpha-1-subunit containing integrins. In particular, the antagonists are antibodies specific for VLA-1 (very late antigen.) alpha-1-beta-1 integrin) or VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the integrin and tis cognate ligand (collagen IV, and laminin in the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4). The method of the invention may be used to treat chronic renal failure, end-stage renal disease, chronic diabetic nephropathy, diabetic collagens of your pretrensive glomerulosclarosis, chronic glomerulomphitis, hereditary nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent fibronectin, which inhibit fibronectin-dependent call adhesion, and may therefore be used in the method of the invention.
                                                                                                                                                                                                                                 Treating a mammal in, or at a risk of developing, chronic renal failure, involves administering at least one integrin antagonist to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibronectin fragment and fibrin related peptide SEQ ID NO:1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 23; DB 22; Length 5; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                (BIOJ ) BIOGEN INC.
(UNLO ) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 24; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB91966 standard; Peptide; 5 AA.
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99US-0153406.
99US-0159783.
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                      99US-0153826
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                                                                                                                                                                                     WPI; 2001-273408/28
                                                                                                                                        Allen A, Pusey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5 AA;
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10-SEP-1999;
15-OCT-1999;
                      14-SEP-1999;
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                                                                                                                                                                                                                                                                                        mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives and related compounds (1), and their scalylalkanoic acid derivatives and related compounds (1), and their salely for salts and prodrugs. These are are integrin inhibitors, specificially of VLA-4 (very late antigen 4, also known as alpha 4-beta-1 or CD494/CD29), which mediate cell adhesion. VLA-4 is a receptor for the cytokine-finducible cell surface protein VCAM-1 (vascular cell adhesion molecule-1) and for the alternatively spliced forms of fibronectin (FN) which contain the CS-1 domain. The novel compounds inhibit cell adhesion, and consequent or associated pathogenic processes mediated by VLA-4, and may therefore be useful in the treatment and prevention of inflammatory, autoimmune, or respiratory disorders. These include asthma, arthritis, psoriasis, multiple sclerosis, transplant rejection, diabetes, and disease. Sequences AAVS048-VS050 represent peptides derived from the VLA-4-binding domain of the FN CS-1 region which contain the LDV motif and are known to inhibit fibronectin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Integrin antagonist, VLA-4 antagonist, alpha-4-beta-1 integrin, very late antigen; antibody, kidney disease; chronic renal failure, end-stage renal disease; chronic diabetic nephropathy; diabetic glomerulopathy; diabetic renal hypertrophy; hypertensive nephrosclerosis; hypertensive glomerulosclerosis; chronic glomerulonephritis; hareditary nephritis; renal dysplasia; nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                               Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5;
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibronectin VLA-4 binding domain-derived pentapeptide #1.
                                                                                                                                                                                                                                                                                   Duplantier AJ, Milici AJ, Chupak LS
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 2; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB73465 standard; peptide; 5 AA.
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                                                                                                                                        99WO-IB00973.
                                                                                                                                                                                       98US-0091180
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Best Local Similarity 100.v.
Files 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001 (first entry)
                                                                                                                                                                                                                                      (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                  WPI; 2000-126762/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AA;
                                            WO200000477-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell adhesion.
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                                                                                                                                        31-MAY-1999;
                                                                                                                                                                                       30-JUN-1998;
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                                                                                           06-JAN-2000
Synthetic.
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RESULT 8 AAB7346

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27-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                           1 EILDV
                                                                                                                                                                                                                                                                                                                                                                            1 EILDV
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                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide components to form a peptidase stabilised therapeutic peptide components to form a city are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 aminos, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases in the action of AMB02441 represent peptides which can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                   Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                        Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                            Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 22; 100.0%; Pred. No. 7.8e+05;
                      Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                               exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin recognition peptide sequence #3.
                                                                                                                  Disclosure; Page 569; 733pp; English.
                        Milner PG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfaff M,
                        Bridon DP, Ezrin AM,
(CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Then 5; Conserve
                                               WPI; 2001-112059/12.
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                                                                                                                                                                                                                                                                                                                                                     s AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                         EILDV
                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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The present sequence is given in a specification relating to a polypeptide comprising a series of heptad-repeats that mimic a transmembrane domain, and a selected cytoplasmic domain attached to the putpad repeats. At least a portion of the polypeptide is prepared recombinantly or at least 1 heptad repeat in the series has a different amino acid sequence to other heptad repeats in the series. The collypeptide is useful in the construction of structural models which are useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein having the selected cytoplasmic domain and for identifying therapeutic compounds. It is also useful for and for identifying agents as inhibitors of alpha4 integrin biological responses by contacting the structural model with paxillin or a paxillin related molecule in the presence and absence of a test agent and determining binding of paxillin related molecule to the structural model. A decrease in binding in the presence of the test agent indicates that the test agent is an inhibitor of alpha4 integrin blocking immune responses in conditions such as inflammatory bowel disease, arthritis, multiple sclerosis and asthma and in inhibiting atherosclerosis and scarring during wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
mimic a transmembrane domain and cytoplasmic domain attached to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deptad repeat; transmembrane domain; cytoplasmic; integrin;
inflammation; thrombosis; malignancy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #3 recognised by integrin.
                                                                                                                  Disclosure, Page 2; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 2; 36pp; English
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                                          heptad repeats
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The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN/VLA-4 interaction plays and runcortion may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, cliabetes, inflammatory bowel disease, kidney inflammation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and cardiovascular disorders
The present invention relates to a peptide with a series of heptad-repeats that mimic a transmembrane domain and a selected cytoplasmic domain attached to the heptad respeats. The invention is useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein with the selected cytoplasmic domain and for identifying therapeutic compounds. It is also useful for identifying a cytoplasmic domain binding partner. It is may be used to study protein interactions with transmembrane proteins such as integrin, which can be used to treat conditions in which over activity of integrins is involved, such as inflammation,
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen PG;
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                       Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huyghe BG,
                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 22; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      He Y,
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibronectin CS1-derived peptide #34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY77443 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US26605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0113689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arrhenius TS, Elices MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                             thrombosis and malignancy
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                              WPI; 2000-182213/16.
                                                                                                                                                                                                                                  5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200002903-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CYTE-) CYTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-2000
                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY77443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4 mediated important role in the maturation and trafficking. VLA-4 mediated control important role in the maturation and reafficking. VLA-4 mediated control important role in the inflammatory response. The peptidomimetics of the critical step in the inflammatory response. The peptidomimetics of the critical step in the inflammatory response. The peptidomimetics of the conditions, such as sathma, rheumatoria arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriants and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, diabetes, inflammatory bowel disease, kidney inflammation and restences of view of the central nervous contaction and restences.
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restenosis. Prior art inhibition of VLA-4/CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414 and AAY77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and cardiovascular disorders
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen PG;
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                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 21; Length 6; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huyghe BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibronectin CS1-derived peptide #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY77444 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-182213/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                            6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          2 EILDV
                                                                                                                                                                                                (AAY77410)
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY77444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia.
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Matches
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Gaps

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Indels

Length 7;

Score 23; DB 19; Pred. No. 7.8e+05; 0; Mismatches

100.0%;

Conservative

Query Match Best Local Similarity Matches 5; Conserv

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involves the use of anti-VLA-4 antibodies, which can themselves induce ar immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to and AX777434 *Y77444 represent fragments of the CS-1 peptide tested for the comparison to the CS-1 peptide and therefore less expensive to the Late and AX777434 *Y77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an alpha4 integrins targeting sequence, which is used in an example from the present invention. The present invention describes a chimeric adenovirus fibre protein (AFP) containing a constrained non-native amino acid sequence. The non-native amino acid sequence allows the chimeric fibre (or a vector comprising the chimeric fibre) to more efficiently bind to and enter cells. The products can be used for gene therapy, for treating cancer, e.g. melanoma, glioma and lung cancers as well as genetic disorders, e.g. oystic fibrosis, haemophilia and muscular dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g. prevent restenosis following angioplasty or to promote angiogenesis to reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric; adenovirus; fiber protein; binding; targeting; coat protein; constrained peptide motif; gene therapy; cancer; heart disease; autoimmune disorder.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric adenovirus fibre proteins - containing non-native amino acid sequence to provide for binding and entry into cells, especially for gene therapy
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                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                             100.0%; Score 23; DB 21; 100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW56065 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                          Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kovesdi I, Roelvink PW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-169169/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENV-) GENVEC INC.
                                                                                                                                                                                          6 AA;
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Mastadenovirus.
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                                                                                                                                                      (AAY77410).
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Fibronectin; extracellular matrix receptor; ECMR: type III; connecting segment; IIICS; adhesion; alpha4beta1; lymphocyte; autoimmune disease; allergy; asthma; ligand.

89US-0402389. 90WO-US04978

31-AUG-1990; 01-SEP-1989;

WO9103252-A 21-MAR-1991

Synthetic.

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(WAYN/) WAYNER

Wayner E;

Peptide #352 derived from Cs-1 peptide of IIICS region.

(first entry)

04-JUN-1991

AAR11361;

AAR11361 standard; peptide; 8 AA.

RESULT 15

AAR11361

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                                                                                                                                                                                                                                                                                                                          Inhibition of lymphocyte adherence to vascular endothelium - using a novel antibody or peptide for treatment of auto-immune disease, asthma, allergy etc.
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100.0%; Pred. No. 7.8e+05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 74; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR28885 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                   WPI; 1991-101865/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA;
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Matches
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ID AAR2
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Sequence

us-09-251-073a-16.open.rag

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92JP-0271293.
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94US-0273055.
                                                                  92JP-0271293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLA-4 binding peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                      WPI; 1994-173758/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA;
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 JP06116288-A.
                                                                                                  09-OCT-1992;
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11-JUL-1994;
                                                                  09-OCT-1992;
                                 26-APR-1994.
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                                                                                                                                                                                                                                 FIGURE 1. THE PROOF CHISTON AND THE METERS TO THE TOTAL CHISTON AND THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE METERS TO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAR28885-86 are peptides which have been shown to inhibit cell adhesion. These peptides can be used as the active component in a cancer metastasis inhibitor, a wound healer, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressant, a platelet aggregation inhibitor or a neuropathy
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                                                                                                Cell adhesion, cancer; metastasis inhibitor; wound healer; immunosuppressant; platelet; aggregation inhibitor; neuropathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propenamide; cell adhesion antagonist; anticancer; antitumour; lymphocyte activation; metastasis; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide deriv. - useful as cancer metastasis inhibitor, wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 13; Length 8; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                      "Terminal Glu residue is linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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optically active
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                                                                Cell adhesion inhibitory peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nealer, immunosuppressant, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FUJF ) FUJI PHOTO FILM CO LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-395376/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA;
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Modified-site
                                                                                                                                                                                        Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                              JP04295497-A
                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1991;
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                                23-MAR-1993
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AAR28885;
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VLA-4; inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR; alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis; complementarity determining region; inflammatory brain disorder; therapy; multiple aclerosis; encephalitis; Alzheimer's disease; atherosclerosis; AlDS dementia; diabetes; inflammatory bowel disease; tumour metastasses; rheumatoid arthritis; transplant rejection; myocardial ischaemla; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new propenamide compounds of formula RIR2C=C(R3)CO-(NH)x-A and their (optionally crosslinked) polymers, where R1 and R2 are H or COOH, R3 = H, Me, Et, halo or carboxymethyl, A is a peptide of formula -(R4)x-(CO)x-(G1U)x-(IL8)x-Leu-App-Val-(Pro)x-(Ser)x-(Thr)Xin-(Z)x-(R5)x-, where Z = 0 or NH, one of R4 and R5 is a terminal H and the other is absent or 1-11C alkylene or 6-11C arylene each of which may be optionally substituted, n = 1 - 5, and x = 0 or 1. The compounds and their polymers combine with cell surface receptors and prevent cell adhesion. They can be used to inhibit cancer metastasis and to activate lymphocytes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                            New propenamide cpds. which are N-substd. by specified peptide, and new polymers - are cell adhesion inhibitors useful e.g. for preventing cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           components of cell culture substrates.
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                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2; 8pp; Japanese.
(FUJF ) FUJI PHOTO FILM CO LTD
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AAW25187-W25192 are peptides containing an LDV sequence or equivalent. The peptides are capable of binding to cell adhesion molecules and are used in aqueous irrigation solutions for use during and after endoscopic operations Preferred irrigation solutions are electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid acide). The solutions are especially used for irrigating the bladder during and after tumour removal by transurethral resection. The peptides protect against recurrence of tumours.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               introducing genetic material, proteins, peptides and immunoglobulins into living cells. In particular, they can be used in gene therapy for the treatment of disorders such as thalassemia and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-viral; immobilisation; microinjection; gene therapy; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides AAW63133-34 appear in the specification, which describes non-viral mediated methods for incorporating a macromolecule into a cell. The methods and products permit the immobilisation microinjection and recovery of cells. The methods can be used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-viral incorporation of molecules into cells - by treating surface with adhesive molecule, contacting with cells and introducing molecules by, e.g. micro:injection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
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                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 18; 100.0%; Pred. No. 7.8e+05;
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llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide sequence of the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW63133 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENESYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thallasemia; cancer.
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                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             1 EILDV 5
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                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                            AAR92536-R92555 represents VLA-4 binding peptides derived from the antibody 21/6. VLA-4 is also known as alpha4betal integrin and cantibody 21/6. VLA-4 binds to the non-matrix molecule VCAM-1, which is expressed by endothalial and other cells. These sequences mimic a short consensus sequence in the heavy chain complementarity determining region (CDR) 3 of monoclonal antibodies against alpha4betal integrin. These sequences inhibit the adhesion of leucocytes mediated by VLA-4. It is useful for treating inflammatory brain disorders (especially multiple sederosis), meningitis, encephalitis, asthma, Alzheimer's disease, theumatord arthritis, transplant rejection, tumour metastases and myocardial ischaemia. These sequences can also be labelled, and can then the used for in vivo or in vitro diagnosis, such as monitoring confidential metastases, inflammatory responses, isolating leucocytes, in assays for inhibitors of inflammatory responses, isolating leucocytes, in assays for inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                 New peptide(s) that bind VLA-4, inhibit leucocyte adhesion - useful esp. for treatment of inflammatory disease, e.g. multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDV; leucine; aspartic acid; valine; cell adhesion molecule; binding; bladder irrigation; tumour removal; endoscopic operation; transurethral resection; cancer; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contg. peptide(s) that bind to cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory responses, isolating leucocytes, in assays for VLA-4/VCAM-1 interactions and imaging sites of inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 17; Length 8; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDV-peptide capable of binding cell adhesion molecules.
                                               Yednock TA;
                                                                                                                                                                                                Example 7; Page 26; 42pp; English.
  (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW25190 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endoscopic irrigation solns. adhesion molecules
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Matches 5; Conservative
                                           Pleiss MA, Thorsett ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FREP ) FRESENIUS AG
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This sequence represents a fibronectin protein fragment used in the extracellular matrix (A) of the invention. (A) is used for promoting wound healing, and comprises a recombinant fibronectin peptide, containing peptide fragments from at least two fibronectin domains, and a backbone matrix. The fibronectin domain peptides used are preferably from the IIICS domain. The cell binding domain, or the heparin II binding domain, or the heparin II binding domain of human fibronectin. (A) provides haemostasis and an environment that recruits new tissue cells to the site of the wound. (A) is used to promote healing of acute or chronic wounds, e.g. surgical incisional promise, traumatic wounds, radiation wounds, cancer extirpations, venous leg ulcers, diabetic ulcers and pressure ulcers.
          Fibronectin, extracellular matrix; wound healing promoter; IIICS domain; cell binding domain; heparin II binding domain; haemostasis; therapy; surgical incisional wound; traumatic wound; radiation wound; cancer extirpation; venous leg ulcer; diabetic ulcer; pressure ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibronectin; extracellular matrix. open wound healing; IIICS domain; acute gaping cutaneous wound; chronic cutaneous ulcer; therapy; wound healing promoter; cell binding domain; heparin II binding domain.
                                                                                                                                                                                                                                                                                                                                                          Extracellular matrix for promoting wound healing containing recombinant fibronectin-derived peptide and backbone matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 20; Length 8; ilarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibronectin protein IIICS domain peptide.
                                                                                                                                                                                                                                                           (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                           Greiling D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32874 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                           WPI; 1999-527421/44
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-1999;
                                                                                                                              WO9942126-A1
                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                           Clark RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a specifically claimed non-native amino acid sequence from a chimeric adenovirus fibre protein (AFP) of the present invention. The non-native amino acid sequence allows the chimeric fibre (or a vector comprising the chimeric fibre) to more efficiently bind to and enter cells. The products can be used for gene efficiently bind to and enter cells. The products can be used for gene well as genetic disorders, e.g. metanonma, glioma and lung cancers as well as genetic disorders, e.g. cystic fibrosis, haemophilia and muscular dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g. prevent restenosis following angioplasty or to promote angiogenesis to reperfuse necrocitic tissue, and in autolimmune disorders, e.g. Crohn's disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
                                                                                                                                                                                                        Chimeric; adenovirus; fiber protein; binding; targeting; coat protein; constrained peptide motif; gene therapy; cancer; heart disease; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                               Chimeric adenovirus fiber protein non-native amino acid sequence 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric adenovirus fibre proteins - containing non-native amino acid sequence to provide for binding and entry into cells, especially for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 19;
100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 84; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY32862 standard; peptide; 8 AA
                                                                               AAW56046 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                           97WO-US14719
                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0701124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-169169/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA;
                                                                                                                                                                                                                                                                                             Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
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 1 EILDV
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                                                                                                               AAW56046;
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                                                RESULT 21
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(UYNC-) UNIV NORTH CAROLINA.
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                         Boucher RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EILDV
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                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                               cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY80489
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                                                                                                                                                This sequence represents a fibronectin protein fragment used in the extracellular matrix of the invention. The extracellular matrix comprises two or more fibronectin domains in a backbone matrix, and is used to enhance wound healing. The fibronectin domain peptides used are preferably from the IIICS domain, the cell binding domain, or the heparin II binding domain of human fibronectin. The matrix facilitates wound healing by providing an environment that intrinsically recruits new tissue cells to the wound site. The new matrix is useful for facilitating wound healing, especially useful for treating open wounds such as acute gaping cutaneous wounds and chronic cutaneous ulcers. The problem of chronic, non-healing wounds is severe. These open wounds require long-term care and procedures that are costly and labour intensive.

The prior compositions and matrices have not been useful or cost effective. The present invention provides a matrix for wound healing that meets these requirements, and overcomes the deficiencies of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition; gene therapy; junctional complex disruption; cytostatic; cardiant; vasotropic; antiinflammatory; antilipaemic; cytostatic; inflammatory disease; fibrotic lung disease; peripheral vascular disease; coronary arterial disease; restenosis; hypercholesterolaemia; cancer; human; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                      New extracellular matrix used to accelerate healing of acute gaping cutaneous wounds and chronic cutaneous ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vitronectin peptide used to enhance viral vector binding affinity.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 20; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
          (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB35734 standard; peptide; 8 AA.
                                                                                                                           Claim 5; Page 19; 43pp; English
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99GB-0009073.
99GB-0009297.
99US-0153757.
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Best Local Similarity
5; Conserve
                                                             WPI; 1999-527415/44.
                                                                                                                                                                                                                                                                                                                                                                                         8 AA;
                                                                                                                                                                                                                                                                                                                                                                  prior matrices
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20-APR-1999;
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13-SEP-1999
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                                    Clark RA,
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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therapy, comprising a nucleic acid encoding a therapeutic gene and a promoter, a transfection vehicle and an agent to disrupt the function of the junctional complex in the cells. The pharmaceutical composition has cytostatic, cardiant, vasotropic, antinflammacory and antilipaemic activity. The pharmaceutical composition is useful for gene therapy and for enhancing efficiency of gene delivery to cells. The composition is useful for gene therapy of experic fibrosis, inflammatory or fibrotic lung diseases, peripheral vascular disease, coronary arterial diseases, restenosis, hypercholesterolaemia and cancer. The present sequence represents a vitronectin peptide. The peptide can be used to enhance the binding affinity of a viral vector used in the pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       System for reconstructing osseous tissue, useful e.g. for treating fractures, comprises scaffold containing promoter of bone formation and
                                                                                 Novel pharmaceutical composition useful for gene therapy, comprises nucleic acid encoding therapeutic gene and a promoter, transfection vehicle and an agent which disrupts function of junctional complex in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bone regenerative, osteopathic, osseous tissue, reconstitution, scaffold matrix, bone formation promoter; bone resorption inhibitor, cell adhesion; osteoblast, osteoclast; bone defect; fracture.
                                                                                                                                                                                                                                               This invention relates to a pharmaceutical composition used for gene
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Pred. No. 7.8e+05;
Man Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
                                                                                                                                                                                                Disclosure; Page 12; 51pp; English.
Johnson LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY80489 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   composition of the invention.
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inhibitor of bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US16800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.00
These 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell adhesion peptide #24.
Ford MJ,
                                       WPI; 2000-679557/66.
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The invention relates to novel arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives and related compounds (I), and their salts and prodrugs. These are are integrin inhibitors, specifically of VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD494(CD29), which mediate cell adhesion. VLA-4 is a receptor for the cytokine-inducible cell surface protein VCA-1 (vescular cell adhesion molecule-1) and for the alternatively spliced forms of fibronectin (FN) which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
                                                                                                                                                                                                                                                                                           AAY69618 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                VLA-4 inhibitor peptide #1.
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PFIZ ) PFIZER PROD INC.
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                                                                                                                                                                                               Local Similarity
nes 5, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                            AAY69618;
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                                                                                               bone formation and a component that decreases bone resorption [11].

(II) induces migration and adhesion of osteoblasts and osteoclasts and control of induces migration and adhesion of osteoblasts and osteoclasts and rearrix. (I) is preferably selected from: selectin or selectin binding fragments, proteins and peptides that facilitate cell adhesion, companinogen activator inhibitors, protease inhibitors and metalloprocease inhibitors. The peptides AAY80466-Y80492 are claimed examples of cell adhesion peptides used in the system of the invention. The system is used to replace, remodel or correct bone defects, e.g. fractures, fissures or bone mass loss. Incorporation of (I) into the scaffold results in rapid seeding by osteoblasts and the development of an organic matrix, i.e. the preformed scaffold replaces the scaffold can extenderemining step of extracellular matrix formation. The scaffold can be designed to have a predetermined resorbiton/degradation rate, and may
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                      ention relates to a novel system for reconstitution of ossec comprising a scaffold carrying a compound (1) that promotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 21; Length 8; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               include regulatory compounds for specific cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 2; 120pp; English.
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and consequent or associated pathogenic processes mediated by VLA-4, and way therefore be useful in the treatment and prevention of inflammatory, autoimmune, or respiratory disorders . These include asthma, arthritis, psoriasis, multiple sclerosis, transplant rejection, diabetes, and inflammatory bowel disease. Sequences ANY69618-Y69520 represent peptides derived from the VLA-4-binding domain of the FN CS-1 region which contain the LDV motif and are known to inhibit fibronectin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating a mammal in, or at a risk of developing, chronic renal failure, involves administering at least one integrin antagonist to the
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin; very late antigen; antibody; kidney disease; chronic renal fallure; end-stage renal disease; chronic diabetic nephropathy; diabetic chronic glomerulopathy; diabetic renal hypertrophy; hypertensive aphroscalcaosis; hypertensive alomerulonephritis; hereditary nephritis; hereditary nephritis; nenal dysplasis; nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
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                                                                                                                                                                                                                          Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibronectin VLA-4 binding domain-derived octapeptide.
                                                                                                                                                                                                                          Score 23; DB 21;
Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73464 standard; peptide; 8 AA.
                                                                                                                                                                                                                            100.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOJ ) BIOGEN INC
                                                                                                                                                                                    8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200119396-A1
                                                                                                                                                 cell adhesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
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                                                                                                                                                                                                                                                                                                           EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB73464;
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammal
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exemplification of the present invention
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                               Sequence
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                                                                                                                                                                                     RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of the perfect than from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular upcake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the
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glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis, hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent peptides derived from the VLA-4 binding domain (CS-1 region) of fibronectin, which inhibit fibronectin-dependent cell adhesion, and may therefore be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Protection, endogenous therapeutic peptide; peptidase, conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                  Fibronectin fragment and fibrin related peptide SEQ ID NO:1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thibaudeau K;
                                                                                                                           100.0%; Score 23; DB 22; Length 8; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 569; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bridon DP, Ezrin AM, Milner PG,
                                                                                                                                                                                                                                                                                  AAB91967 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0134406.
99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC.
                                                                                                           WPI; 2001-112059/12.
                                                                                                  8 AA;
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10-SEP-1999;
15-OCT-1999;
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                                                                                                  Sequence
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                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One of 1 or 2 of these chains are attached via the N- or C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide(s) contg. PEG derivs. - are cell adhesion and platelet adhesion inhibitors, useful as carcinoma metastasis inhibitors, immuno-regulators and for wound healing
                                          Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                  Indels
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                                        100.0%; Score 23; DB 22;
llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triazine; polyethylene glycol; agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 3; 11pp; Japanese.
                                                                                                                                                                                                                                                                             AAR29631 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR30433 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                              Adhesion inhibitor peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity luv...
5; Conservative
                 Query Match
Best Local Similarity
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8 AA;
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The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD494/CD29) to the CS-1 portion (55 amino acida) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an leukocyte adhesion to the CS-1 FN/VLA-4 interaction plays an elukocyte adhesion to the CS-1 FN of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatoid arthritis is osteoarthritis and allograft rejection. They may also be used to treat poorianis and other skin inflammations, demyelinating diseases of the central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibronectin, FN; CS-1; endothelial cell, VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and cardiovascular disorders
                                                                                                         The sequences given in AAR28885-86 are peptides which have been shown to inhibit cell adhesion. These peptides can be used as the active component in a cancer metaeris inhibitor, a wound healer, an immunosuppressant, a platelet aggregation inhibitor or a neuropathy
                                      Peptide deriv. - useful as cancer metastasis inhibitor, wound healer, immunosuppressant, etc.
                                                                                                                                                                                                                   100.0%; Score 23; DB 13;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibronectin CS1-derived peptide #27
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                                                                                                                                                                                                                                                                                                                                                                        AAY77436 standard; peptide; 9 AA.
                                                                                 Claim 1; Page 2; 10pp; Japanese
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                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                         9 AA;
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EILDV
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                                                                                                                                                                 treating
                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                          This sequence represents an animal cell adhesion peptide. It is useful as an animal cell adhesion inhibitor or platelet aggregation/adhesion inhibitor.
                                                                                                                                                                                                                                                           New polypepitide(s) contg. repeat units of octa:peptide(s) - for inhibiting adhesion of cells (e.g. to fibronectin) and aggregation adhesion of platelets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell adhesion; cancer; metastasis inhibitor; wound healer; lmmunosuppressant; platelet; aggregation inhibitor; neuropathy.
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                         platelet aggregation inhibitor; platelet adhesion inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell adhesion inhibitory peptide #2.
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                                                                                                                                                                                                                                                                                                                 Disclosure, Page 1, 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR28886 standard; peptide; 9 AA.
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                                                                                                                                                                                                      (FUJF ) FUJI PHOTO FILM CO LTD
                                                                                                                                                                            90JP-0326224
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Cell adhesion inhibitor #2.
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                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
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Modified-site
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                                                                                            JP04198194-A
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                                                                                                                                                 28-NOV-1990;
                                                                                                                                                                            28-NOV-1990;
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                                         fibronectin
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                                                                 Synthetic.
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(e.g., multiple sclerosis), allergies, atherosclerosis, colitis, diabetes, inflammatory bowel disease, kidney inflammation and restenosis. Prior art inhibition of VLA-4CS-1 interaction either involves the use of anti-VTA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidemineties of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to anniantacture, and are resistent to proteolysis. Sequences AA777411-Y77414 and AA777434-Y77444 represent fragments of the CS-1 peptide for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, D494/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes, the CS-1 FN/VLA-4 interaction plays an lemportant role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory conditions, such as astbma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyeliating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 21; Length 9
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibronectin CS1-derived peptide #28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY77437 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    9 AA;
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The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD94/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein (ibronectin (FN). VLA-4 is expressed on the surface of leukcoytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4 mediated elukcoyte adhesion to the CS-1 FN/VLA-4 interaction plays an elukcoyte adhesion to the CS-1 FN of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the cinvention may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other expression and inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, cliabetes, inflammatory bowel disease, kidney inflammation and
diabetes, inflammatory bowel disease, kidney inflammation and restenosis. Prior art inhibition of VLA-4/CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteclytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to proteclysis. Sequences AAY77411-Y77414 and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
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                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 21;
ilarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibronectin CS1-derived peptide #29.
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Matches 5; Conserv
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The invention relates to peptidomimetic compounds (AAY77415-Y77438)
capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD940/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammacory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, diabetes, inflammatory bowel disease, kidney inflammation and restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
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restenosis. Prior art inhibition of VLA-4/CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to proteolysis. Sequences AAX77411-Y77414 and AAX77434-Y77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 21; Length 9; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Indels
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involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistent to proteolysis. Sequences AAY77411-Y77414 and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a 2,4,6-trisubstituted s-triazine ring, where one substitution is a polyethylene glycol chain [CH3 (CH2CH2)] no-6 - no-1-50)] and the cher is either another, same, polyethylene glycol chain, or another, same, peptide chain. For examples see also AAR29631-32. These PEG derivates or their salts are useful as animal cell adhesion inhibitors, or as platelet agglutination or adhesion inhibitors. They may also be used as carcinoma metastasis inhibitors, wound healing drugs and
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                                                                                                                                                                                                     Length 9;
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                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                           100.0%; Score 23; DB 21;
ilarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triazine; polyethylene glycol; agglutination.
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Matches 5; Conserv
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"Any amino acid or absent may also have opt. -O- or -NH- followed by an opt substd. (un) satd. 8-24 C alkyl."

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/note= "Any amino acid or absent
may also have opt -CO- followed by an opt.
substd. (un) satd. 8-24 C alkyl."
wound healing; immune inhibitor; neuropathy drug.
                               Location/Qualifiers
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/note= "
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Misc-difference
                                       Misc-difference
                                                                        Misc-difference
                                                                                                                                                                                                                                    treating drug
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Matches
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Gaps
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                                                                                                                                                                                                 'note= "May be an amino acid, peptide or absent."
                                                                                                                                                                                                                 /note= "May be an amino acid, peptide or absent."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelet aggregation; cell adhesion; cancer metastasis inhibitor;
                                                                                                                                                                                                                                                                                                                                  New polypepitide(s) contg. repeat units of octa:peptide(s) - for inhibiting adhesion of cells (e.g. to fibronectin) and aggregation adhesion of platelets
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                                                                                                                                        platelet aggregation inhibitor; platelet adhesion inhibitor; fibronectin.
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0; Indels
Mismatches
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                                                                        AAR30432 standard; peptide; 10 AA.
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                                                                                                                       Cell adhesion inhibitor #1
                                                                                                        (first entry)
Conservative
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Best Local Similarity
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Matches
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ID AAR3
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Gaps
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                                                            Peptide deriv., for cancer metastasis inhibitor - useful as wound
healer, immune- and platelet aggregation inhibitor and neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        platelet aggregation; cell adhesion; cancer metastasis inhibitor; wound healing; immune inhibitor; neuropathy drug.
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                                                                                                                                                                                        Claim 1; Page 1; 9pp; Japanese.
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WPI; 1992-401809/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
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             Length 10;
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             13;
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Pred. No. 31;
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                                     0; Mismatches
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             100.0%;
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            Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Misc-difference
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                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                              This peptide deriv. inhibits adhesion of animal cells, partic patchete, aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation inhibitors or drugs for treating neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This peptide deriv. inhibits adhesion of animal cells, partic platelet aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation inhibitors or drugs for treating neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
                                                                                                  Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        platelet aggregation; cell adhesion; cancer metastasis inhibitor; wound healing; immune inhibitor; neuropathy drug.
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                                                                                                                                                    Disclosure, Page 3, 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Platelet aggregation inhibitor #3.
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Best Local Similarity
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treating drug
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26-MAR-1991;
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The alpha-4 beta-1 (CD49d/CD29, VLA-4) cell adhesion receptor is an active participant in leukocyte trafficking functions. Binding of inflammatory cells to endothelial cells that express the CS-1 portion (AAW01703) of fibronectin on their surfaces can be inhibited by CS-1 peptidomimetic cpds. of minimal length. A minimal essential sequence for
                                                                                                                                                                         This peptide deriv. inhibits adhesion of animal cells, partic patelet aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation inhibitors or drugs for treating neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibronectin; high affinity, CS-1; recognition sequence; VLA-4; alpha-4 beta-1 call adhesion receptor; CD94/CD29; inhibitor; leukocyte trafficking function; peptidonimetic; treatment; asthma; rheumatoid arthritis; osteoarthritis; allograft rejection;
                                                                                           Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide mimics of fibronectin CS-1 sequence - inhibit interaction of endothelial cells and VLA-4 carrying inflammatory cells, for treating or preventing asthma, arthritis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skin inflammation; central nervous system demyelinating disease.
                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 13; Length 10; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Standard peptide for VLA-4 binding assay.
                                                                                                                                                  Disclosure; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAW01705 standard; peptide; 10 AA
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                                        (FUJF ) FUJI PHOTO FILM CO LTD
             91JP-0062148.
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93US-0164101
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             26-MAR-1991;
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platelet aggregation; cell adhesion; cancer metastasis inhibitor; wound healing; immune inhibitor; neuropathy drug.
                                                                                          /note= "has CH2CH(CH3)(CH2)3CH(CH3)(CH2)3CH(CH3)--(CO--(CH2)3CH(CH3)2-CO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            platelet aggregation; cell adhesion; cancer metastasis inhibitor; wound healing; immune inhibitor; neuropathy drug.
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-CH(CH3)(CH2)3CH(CH3)2"
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100.0%; Pred. No. 31;
iive 0; Mismatches
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The alpha-4 beta-1 (CD49d/CD29, VLA-4) cell adhesion receptor is an active participant in leukocyte trafficking functions. Binding of inflammatory cells to endothelial cells that express the CS-1 portion (AAMO1703) of fibronectin on their surfaces can be inhibited by CS-1 peptidomimetic cpds. of minimal length. A minimal essential sequence for peptidomimetic cpds. of minimal length. A minimal essential sequence for beptidomimetic peptidomimetic the binding of Jurkat cells (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay in an aq. buffer at a pH value of 7.2-7.4 to an extent that is equal to or upto about 3000-fold greater than the inhibition in the binding exhibited by AAMO1705. CS-1 mediated inflammation, e.g. asthma, rheumatoid arthritis, osteoarthritis, allograft rejection, skin
specific VLA-4 recognition of CS-1 has been identified as the tripeptide LDV. The generic peptidomimetic inhibits the binding of Jurkat cells (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay in an aq. buffer at a pH value of 7.2-7.4 to an extent that is equal to or upto about 3000-fold greater than the inhibition in the binding exhibited by the present standard peptide sequence. CS-1 mediated inflammation, e.g. asthma, rheumatoid archritis, osteoarthritis, allograft rejection, skin inflammation or central nervous system demyelinating disease, can be treated by the peptidomimetics. See AAW01706-27 for exemplary inhibitor peptides.
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              fibronectin; high affinity; CS-1; recognition sequence; VLA-4; alpha-4 beta-1 cell adheaion receptor; CD49d/CD29; inhibitor; leukocyte trafficking function; peptidomimetic; treatment; asthma; rheumatoid arthritis; osteoarthritis; allograft rejection; skin inflammation; central nervous system demyelinating disease.
                                                                                                                                                                                                                                                                                                                                                                                                       Inhibitor of fibronectin CS-1 peptide and VLA-4 receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide mimics of fibronectin CS-1 sequence - inhibit interaction of endothelial cells and VLA-4, carrying inflammatory cells, for treating or preventing asthma, arthritis etc.
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                                                                                                                                                                           100.0%; Score 23; DB, 16; Length 10; 100.0%; Pred. No. 31;
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                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 36; 103pp; English.
                                                                                                                                                                                                                                                                                                                        AAW01725 standard; peptide; 10 AA.
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93US-0164101,
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                                                                                                                                                                                      Local Similarity 100.
Nes 5; Conservative
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                                                                                                                                                  10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arrhenius TS,
                                                                                                                                                                                                                              1 BILDV 5
                                                                                                                                                                                                                                                       3 EILDV 7
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06-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                    AAW01725;
                                                                                                                                                                           Query Match
                                                                                                                                                                                                     Matches
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Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the surface of endothelial cells that line the interior wall of capillaries. VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA481) or VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA481) or VLA-4 for very late antigan-4), a heterodimeric protein present on the surface of certain white blood cells in adhere to the capillary wall in areas where the tissue surrounding the capillary has been infected or damaged. Sometimes this white blood cells flooding to the scene, causing widespread tissue damage. Chods capable of blocking this process may be beneficial as therapeutic agents. IA481 also recognises the extracellular matrix glycoprocein fibronectin. Three distinct IA481-binding sites have been identified within fibronectin. One site is found in the Hepli region and is expressed in all isoforms; two others (CS1 and CS5) are present in the affinity for IA481 and contains the tripeptide LDV as its minimal active site. Peptides AAR95704-805 are modeled after a portion of the CS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4; inhibitor; binding; white blood cell; migration; capillary wall; tissue damage; injury; fibronectin; extracellular matrix glycoprotein; CS1; CS5; H1; LDV; active site.
                                                                                                                                                                                                                                     Gape
inflammation or central nervous system demyelinating disease, can bo
treated by the peptidomimetics. AAW01706-27 are exemplary inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - used for
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                                                                                                                                                                              16; Length 10
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                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-4Beta-1 integrin binding inhibitory peptide 101.
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                                                                                                                                                                           100.0%; Score 23; DB
100.0%; Pred. No. 31;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR95804 standard; peptide; 10 AA.
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                                                                                                                                                                                                      Local Similarity 100.
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                                                                                                                       10 AA;
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Modified-site
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                                                             peptides
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Matches
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Pred. No.

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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guences AAW70543 to AAW70545 represent CS-1 peptide fragments used during the course of the invention. The invention provides integrinting the course of the invention. The invention provides integrinting the course of the invention. The invention provides that comprise an integrint alpha or beta clain associated with an immunoglobulin light or heavy chain. These chimeric proteins form heterodimer complexes, in particular with a chimeric protein containing an integrin alpha chain of an immunoglobulin chain; the immunoglobulin chain; the integrin alpha chain is preferably alpha 4 or alpha 2 and the integrin beta chain is preferably beta 1. Animal cells transformed with vectors containing the DNA coding for the above chimeric proteins can be used in the preparation of the chimeric proteins and their perparation of the chimeric proteins and their betaching promoters and inhibitors of the binding of integrins to their poptential promoters and inhibitors of the binding of integrins to their conjugands, function as blood platelet substitutes and hemostatics and as
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                                                                                                                                                                                                                                                                                               Integrin; alpha-4 chain; immunoglobulin; chimeric; heterodimer complex;
inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
peptide that include the LDV domain presented in such a way by its novel flanking sequence to produce a potent inhibitor of IA4B1 binding.
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin-immunoglobulin chimeric protein heterodimer complexes as ablatelet substitutes - contain the alpha and beta integrin chains associated in stable state and bind to extracellular matrix in the presence of plasma components
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                                                            100.0%; Score 23; DB 17; Length 10; 100.0%; Pred. No. 31; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                       CS-1 peptide fragment 1 (a fibronectin fragment).
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                                                                                                                                                                                               AAW70543 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-JP00370
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                                                                                                                                                                                                                                                (first entry)
                                                 Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TORA ) TORAY IND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanaka T;
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                                                                                                                                                                                                                                                                                                                       CS-1; fibronectin
                                     10 AA;
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                                                                                                                               BILDV
                                                                                                            1 EILDV
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                                   Sequence
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DB 19; Length 10;

100.0%; Score 23;

Query Match

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                                                                                                                                                                                                                                                                                                                              Hepatitis drug; integrin inhibitor; integrin binding; {\tt VLA-4}; treatment; hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin inhibitors including antibodies, proteins, nucleic acids, saccharide(s), capable of binding to integrin(s) as active ingredient in remedies - for treating hepatitis, by inhibiting cell
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Pred. No. 31;
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                                                                                                                                                                                     AAW71246 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                             Peptide sequence of the invention.
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Best Local Similarity 100.00
Cinhes 5; Conservative
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  Conservative
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                                      1 EILDV
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WO200192543-A2
                                             Arrhenius TS,
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Matches
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                                                                                                                                                                                                                                                                                                        The present sequence represents part of a CS-1 peptide. The specification describes a cyclic CS-1 peptidommimencic inhibitor peptide, which is water soluble and inhibits the binding of Jurkat cells to a solid-phase bound peptide (AAW88057). The inhibitor peptides are useful for treating fibronectin CS-1 or sVCAM 1/VLA-4 mediated inflammation, esq. asthma, arthritic conditions (e.g. rheumatoid arthritis, osteoarthritis), allograft rejection, skin inflammation and demyelinating diseases of the central nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibronectin, FN, CS-1, endothelial cell, VLA-4 integrin, alpha-4-beta-1, CD49d/CD29; leukocyte, inflammatory cell, inflammation; cell adhesion, inhibitor; peptidomimetic, autoimmune disease, inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                Cyclic inhibitor peptide - useful for treating fibronectin CS-1 or sVCAM-1/VLA-4 mediated inflammation, e.g. asthma and arthritic
                         Cyclic CS-1 peptidomimmetic inhibitor; Jurkat cell binding; fibronectin CS-1 mediated inflammation; rheumatoid arthritis; CXCM 1/VLA-4 mediated inflammation, asthma; arthritic condition; rheumatoid arthritis; allograft rejection; CS-1; skin inflammation, demyelinating disease; central nervous system.
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         CS-1 peptide portion.
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ses 5; Conservat
                                                                                                                                                                                                                               WPI; 1999-152837/13
                                                                                                                                                                                        (CYTE-) CYTEL CORP.
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                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY77412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 50
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The invention relates to peptidomimetic compounds (AAY77415-Y77438)

Capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CG 6494(CD29) to the CS-1 portion (25 amino acida) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the extracellular matrix protein fibronectin (FN). VLA-4 interaction plays an critical step in the inflammatory endocthelial cells is also a critical step in the inflammatory chronic and acute immunoinflammatory conditions, such as sethma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, clabetes, inflammatory bowel disease, kidney inflammation and crescences, prior art inhibition of VLA-4/CS-1 interaction either response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteclytic degradation. The peptidomimetics of the invention are smaller in CC comparison to the CS-1 peptide and therefore less expensive to comparison to the CS-1 peptide and therefore less expensive to the CS-1 peptide and therefore less expensive to the CS-1 peptide to their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide for (AAY77414).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virucide, human immunodeficiency virus, HIV, cytostatic, ophthalmological, vasotropic, vaccine, gene therapy, transfection, cystic fibrosis, asthma; cancer, lubacemia, glaucoma; gene vaccination, anti-sense therapy, eye disease, corneal organ transplant; integrin;
                                                                                                                                                                                                                                                                New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                     Chen PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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llarity 100.0%; Pred. No. 31;
Conservative 0; Mismatches 0; Indels
                                                                                Huyghe BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transfection associated, integrin binding peptide #8.
                                                                                     He Y,
                                                                                     Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 238; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU74984 standard; Peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                         cardiovascular disorders
                                                                                     Elices
                                                                                                                                                                               WPI; 2000-182213/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 5; Conserv
(CYTE-) CYTEL CORP.
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2000GB-0013089.

2000GB-0013090

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30-MAY-2001; 2001WO-GB02394.
                                                                                             01-MAY-2001; 2001US-287410P.
                                                                                                                       (ICHI-) ICH PRODN LTD
                                                                  30-MAY-2000;
                                                                                  30-MAY-2000;
               06-DEC-2001
                                                                                                                                                  Hart SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR92535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes transfecting (I) confluent cells or other slowly dividing or non-dividing cells that are in contact with each other, with a nucleic acid. The method comprises contacting the cells with a receptor-targeted vector comprising the nucleic acid, and an agent that transfection the section of the useful for transfecting bronchial and lung transfection. (I) is useful for transfection bronchial and lung cancers and viral infections e.g. human immunodeficiency virus (HIV) infection. Hamaropoietic cell transfection enables gene therapy, gene vaccination and anti-sense therapy of diseases involving haematopoietic cells, including leukaemia and bone marrow stem cell disorders.

Transfection of corneal endothelium is useful for treatment of eye classes affecting the corneal organ transplants, for e.g. in glaucoma. A gene preventing cell proliferation in blood vessel walls is introduced using an integrin targeting transfection vector complex (II) to reduce restenosis. (II) is useful for intracellular transport and delivery of anti-sense oligonuclede, which enables antiviral and cancer therapy and is effective in transporting large DNA molecules. This sequence represents a peptide that lacks the conserved RGD integrin binding amino acid sequence but binds integrins allowing the integrin caid to pass into the cell, described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Integrin binding component; polycationic nucleic acid-binding component;
                                                                                                                                                           Transfecting confluent cells with nucleic acid for gene therapy or gene vaccination, comprises contacting the cells with a receptor-targeted vector having the nucleic acid and an agent that disrupts cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lipid component; prophylaxis; immunisation, antisense therapy; asthma; cystic fibrosis; cancer; viral infection; human immunodeficiency virus; HIV infection; vaccines; neuroblastoma; bone marrow stem cell disorder; leukaemia; adjuvant immunotherapy; eye disease; glaucoma; restenosis; integrin-binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 23; Length 10; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                              Claim 17; Page 17; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE17114 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin-binding peptide #16.
30-MAY-2001; 2001WO-GB02396.
                         30-MAY-2000; 2000GB-0013089.
30-MAY-2000; 2000GB-0013090.
01-MAY-2001; 2001US-287410P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                (ICHI-) ICH PRODN LTD
                                                                                                                                    WPI; 2002-114355/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA;
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                                                                                                                                                                                                      unctions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                         Hart SL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE17114
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The invention relates to integrin-targetting vectors having enhanced transfection activity. The vector complex comprises a nucleic acid, an integrin binding component, a polycationic nucleic acid, binding component. The integrin binding component component and a lipid component. The integrin binding component component and a lipid component. The integrin binding component component and a lipid component. The integrin binding component component and a lipid component. The integrin binding element and a spacer element. Complex component acid, for transfecting cells in vitro or in vivo with a nucleic acid, for transfecting bronchial and lung epithelium and caused in human or a non-human animal by a defect and/or a deficiency in a gene, immunisation and antisense therapy of a human or a non-human animal. It is useful for transfections for cystic fibrosis, asthma and also various cancers and viral infections for example human components of neuroblastoma and the effective transfection of primary smooth muscle cells, cardiac myocytes and haematopoietic cells. The manatopoietic cell transfection and the effective transfection of a cytokine gene may be used for adjuvant immunotherapy. Transfection of a cytokine gene may be used for adjuvant immunotherapy. Transfection of a cytokine gene may be used for transfection of corneal and cohem marrow stem cell disorders, for example transfection of corneal and coheminal organ transplants, for example constances and antisense therapy complex of the invention to reduce the present sequence is integrin-binding peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                      has
                                                                   Complex for transfecting cell with nucleic acid for treating, preventing conditions caused by deficiency in a gene in humans, nucleic acid, lipid, integrin binding and polycationic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                       Claim 18; Page 78; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR92535 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Very Match
Best Local Similarity 100.v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLA-4 binding peptide #5.
                                                                                                                                                                                                       acid-binding components
WPI; 2002-139612/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
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Cyclic CS-1 peptidomimimetic inhibitor; Jurkat cell binding; fibronectin CS-1 mediated inflammation; rheumatoid arthritis; sVCAM 1/VLA-4 mediated inflammation; asthma; arthritic condition; rheumatoid arthritis; osteoarthritis; allograft rejection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW88061 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0519109.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B12 peptide sequence.
                                                                          (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 AA;
                                                                                                   Arrhenius TS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-1995;
                                    02-DEC-1994;
                                                 06-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW88061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW88061
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                             ARA92534 and AAR92535 represents VLA-4 binding peptides. VLA-4 is also known as alpha4betal integrin and CD49d/CD29. VLA-4 binds to the non-matrix molecule VCAM-1, which is expressed by endothelial and other cells. This sequence (and peptides designed from it) mimic a short consensus sequence in the heavy chain complementarity determining region (CDR) 3 of monoclonal antibodies against alpha4betal integrin. This sequence inhibits the adhesion of loucocytes mediated by VLA-4. It is useful for treating inflammatory brain disorders (sepecially multiple sclerosis), meningitis, encephalitis, asthma, Alzheimer's disease, rheumatoid arthritis, transplant resjection, tumour metastrases and myocardial ischaemia. This sequence can also be labelled, and can then consensed for in vivo or in vitro diagnosis, such as monitoring inflammatory responses, isolating elecocytes, in assays for inhibitors of VLA-4/VCAM-1 interactions and imaging sites of inflammation.
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             rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma
AIDS dementia; diabetes; inflammatory bowel disease; tumour metastases;
                                                                                                                                                                                                                                                    - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                              esp. for treatment of inflammatory disease, e.g. multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibronectin, high affinity, CS-1, recognition sequence, VLA-4, alpha-4 beta-1 cell adhesion receptor; CD49d/CD29; inhibitor; leukocyte trafficking function; peptidominetic; treatment; asthma; rheumatoid archritis; osteoarchritis; allograft rejection; skin inflammation; central nervous system demyelinating disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 17; Length 11; 100.0%; Pred. No. 35; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                    New peptide(s) that bind VLA-4, inhibit leucocyte adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B12 fibronectin peptide recognition sequence for VLA-4.
                                                                                                                                                                                                    Yednock TA;
                                                                                                                                                                                                                                                                                         Example 5; Page 23; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW01704 standard; peptide; 12 AA.
                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                     95US-0467580.
94US-0273055.
                                                                                                             95WO-US08516.
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                                                                                                                                                                                                    Thorsett ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 5; Conservat
                                                                                                                                                                                                                          WPI; 1996-097452/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 EILDV 8
                                                            WO9601644-A1
                                                                                                             10-JUL-1995;
                                                                                                                                    06-JUN-1995;
11-JUL-1994;
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                                                                                     25-JAN-1996
                                                                                                                                                                                                    Pleiss MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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Gaps

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nervous system.

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This sequence is a fragment of CS-1 (AAW01703) a high affinity peptide cecognition sequence for VLA-4 within fibronectin. The alpha-4 beta-1 (CD494/CD29, VLA-4) cell adheasion receptor is an active participant in leukocyte trafficking functions. Binding of inflammatory cells to endothelial cells that express the CS-1 portion of FN on their surfaces of minimal essential sequence for specific VLA-4 recognition of CS-1 has been identified as the tripeptide LDV. The generic peptidomimetic inhibite the binding of Jurkat cells (ATCC TIB 152) to a solid phase-complete the binding of Jurkat cells (ATCC TIB 152) to a solid phase-complete the inhibition in the binding exhibited by AAW01705. Deletion mutants of the present sequence were formed and in vitro binding of the peptides was assayed and compared to that of the full length CS-1 mediated inflammation, e.g. asthma, rheumatoid archritis, osteoarthritis, allograff rejection, skin inflammation or central nervous system demyelinating disease, can be treated by the peptidomimetics. See AAW01706-27 for exemplary inhibitor peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide mimics of fibronectin CS-1 sequence - inhibit interaction of endothelial cells and VLA-4 carrying inflammatory cells, for treating or preventing asthma, arthritis etc.
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                                                                                                                                                                                                                                                                                                                     Gaeta FCA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 78; 103pp; English.
94WO-US13943.
                                                                                94US-0164101.
93US-0164101.
                                                                                                                                                                                                                                                                                                                          Elices MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Integrin; transfection complex; integrin-binding; lipid; immunisation; antisense therapy, enzyme; therapeutic agent; immunogen; cystic fibrosis; cancer; viral infection; human immunodeficiency virus; cardiovascular;
                                                                                                                                                                  The specification describes a cyclic CS-1 peptidomimimetic inhibitor which is water soluble and inhibits the binding of Jurkat cells to a solid-phase bound peptide (AAW88057). The inhibitor peptides are useful for treating fibronectin CS-1 or sVCAM I/VIA-4 mediated inflammation, e.g. asthma, arthritic conditions (e.g. rheumatoid arthritis, oslograft rejection, skin inflammation and demyelinating diseases of the central nervous system. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                               Cyclic inhibitor peptide - useful for treating fibronectin CS-1 or sVCAM-1/VLA-4 mediated inflammation, e.g. asthma and arthritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New integrin-targeting transfection complex including lipid - used to improve transfection efficiency for a very wide range of cells, useful in, e.g. antisense therapy and genetic immunisation
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                                                Zheng Z;
                                                                                                                                            Disclosure; Columns 77-78; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restenosis; leukaemia; asthma; glaucoma.
                                                Tempczyk A,
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95414 standard; peptide; 12 AA
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94US-0296241
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                                             Arrhenius TS, Elices MJ,
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                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
1es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Integrin-binding peptide
                                                                      WPI; 1999-152837/13.
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                        (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                12 AA;
                                                                                             Cyclic inhibitor
25-AUG-1994;
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AAW9541
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The invention relates to an integrin-targeting transfection complex. The complex comprises a nucleic acid, an integrin-binding component, a

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polycationic nucleic acid-binding component and a lipid. The complexes are used for in vivo or in vitro transfection of cells, specifically:

(1) for treatment or prevention of disease (in humans or other animals) caused by defective or deficient genes; (ii) for immunisation; (iii) for antisense therapy, and (iv) for protein production in host cells, e.g. or enzymes, therapeutic agents, vaccinating immunogens and diagnostic antisens. Typical of the diseases that can be treated or prevented are cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency virus), cardiovascular disease (e.g. restenosis), leuksemia, asthma and glaucoma. Incorporation of the lipid into the complex increases transfection levels from 1-10 percent to over 50 percent. This effect is observed with all cell types tested including those that are resistant to transfection by most plasmid vectors. The complexes can carry large genes, up to 125 kb, e.g. an artificial chromosome. The present sequence represents a claimed example of an integrin-binding peptide used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
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                allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis, allergies, atherocalerosis, colitis, diabetes, inflammatory bowel disease, kidney inflammation and restenosis. Prior art inhibition of VLA-4/CS-1 interaction either immores the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414 and AAY77434-Y77444 represent fragments of the CS-1 peptide to immobility to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes transfecting (I) confluent cells or other slowly dividing or non-dividing cells that are in contact with each other, with a nucleic acid. The method comprises contacting the cells with a receptor-targeted vector comprising the nucleic acid, and an agent that disrupts cell-cell junctions under conditions suitable to effect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transfecting confluent cells with nucleic acid for gene therapy or gene vaccination, comprises contacting the cells with a receptor-targeted vector having the nucleic acid and an agent that disrupts cell-cell
such as asthma, rheumatoid arthritis, osteoarthritis and
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                                                                                                                                                                                                                                                                                          21; Length 12;
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30-MAY-2000; 2000GB-0013090.
01-MAY-2001; 2001US-287410P.
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transfection. (I) is useful for transfecting bronchial and lung epithelium for gene therapy for cystic fibrosis, asthma and also various cancers and vizal infections e.g. human immunodeficiency virus (HIV) infections e.g. human immunodeficiency virus (HIV) infection. Haematopoietic cell transfection enables gene therapy, gene vaccination and anti-sense therapy of diseases involving haematopoietic cells, including leuksemia and bone marrow seem cell disorders.

Transfection of corneal endothelium is useful for treatment of eye disease affecting the cornea or corneal organ transplants, for e.g. in glaucoma. A gene preventing cell proliferation in blood vessel walls is introduced using an integrin targeting transfection in blood vessel and cancer therapy and is effective in transporting large DNA molecules.

This sequence represents a peptide that lacks the conserved RGD cancer therapy and is effective in transporting large DNA molecules.

This sequence represents a peptide that lacks the conserved RGD cancer therapy and of the invention.

Construction of desquence and cysteine residues for cyclisation, but can bind to integrins to allow the nucleic acid to pass into the cell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 23; Length 12; 100.0%; Pred. No. 38;
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30-MAY-2000; 2000GB-0013090.
01-MAY-2001; 2001US-287410P.
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an integrin binding component, a polycationic nucleic acid-binding component and a lipid component. The integrin binding component comprises an integrin-binding element and a spacer element. Complex of the invention is useful for transfecting cells in vitro or in vivo with a nucleic acid, for treatment or prophylaxis of a condition caused in human or a non-human animal by a defect and/or a deficiency in a gene, immunisation and antisense therapy of a human or a non-human animal. It is useful for transfecting bronchial and lung epithelium and corneal endothelium for gene therapy for cystic fibrosis, asthma and calso various cancers and viral infections. It is also useful as a vaccine or for therapy of neuroblastoma and the effective transfection of primary smooth muscle cells, cardiac myocytes and haematopoietic cells. Heematopoietic cell transfection enables gene therapy, gene vaccination and antisense therapy of diseases involving haematopoietic cells. Heematopoietic cell transfection enables gene therapy, gene vaccination and antisense therapy of diseases involving haematopoietic cells. Iransfection enables gene may be used for adjuvant immunotherapy. Transfection of corneal endothelium is useful for treatment of eye disease affecting the cornea or corneal organ transplants, for example in glaucoma. A gene that prevents proliferation of cells in blood vessel walls is introduced using complex of the invention to reduce restenosis. The present sequence is integrin-binding peptide

cetterosis. The present sequence is integrin-binding peptide.
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AAW70541 standard, peptide; 13 AA. (first entry) 26-JAN-1999 AAW70541; RESULT 60 XSXPPPPP

CS-1 peptide sequence (a fibronectin fragment).

Integrin; alpha-4 chain; immunoglobulin; chimeric; heterodimer complex; inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent; CS-1; fibronectin

Synthetic

W09832771-A1

30-JUL-1998.

98WO-JP00370 97JP-0234544 29-JAN-1998; 29-AUG-1997;

(TORA) TORAY IND INC.

97JP-0015118

29-JAN-1997;

Tanaka T; Kainoh M,

WPI; 1998-427881/36.

Integrin-immunoglobulin chimeric protein heterodimer complexes as platelet substitutes - contain the alpha and beta integrin chains associated in stable state and bind to extracellular matrix in the presence of plasma components

Claim 41; Page 25; 87pp; Japanese.

This represents a CS-1 peptide sequence. The invention provides

comprise an integrin alpha or beta chain associated with an

comprise an integrin alpha or beta chain associated with an

comprise an integrin alpha or beta chain associated with an

communoglobulin light or heavy chain. These chimeric proteins form

chercodimer complexes, in particular with a chimeric protein containing

an integrin alpha chain and an immunoglobulin chain with a chimeric

comprise in containing an integrin beta chain and an immunoglobulin chain;

complexes the integrin beta chain is preferably alpha 4

company be a light chain. The integrin alpha chain is preferably alpha 4

com alpha 2 and the integrin beta chain is preferably beta 1. Animal cells

companied with vectors containing the DNA coding for the above chimeric

proteins can be used in the preparation of the chimeric proteins and

chair heterodimer complexes. The heterodimer complexes, which are useful

contesting potential promoters and inhibitors of the binding of

themostatics and as diagnostic agents.

13 AA; Sequence

Gaps ; 100.0%; Score 23; DB 19; Length 13; 100.0%; Pred. No. 42; Indels . 0 0, Mismatches 5; Conservative Query Match Best Local Similarity Matches

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AAW71245 standard; Peptide; 13 AA. 18-NOV-1998 (first entry) AAW71245; 61 RESULT

Peptide sequence of the invention.

Hepatitis drug; integrin inhibitor; integrin binding; VLA-4; treatment; hepatitis.

Synthetic.

WO9837914-A1

03-SEP-1998

98WO-JP00802. 26-FEB-1998; 97JP-0042493. 26-FEB-1997;

(TORA) TORAY IND INC

Tanaka T; Moriya K, Kainoh M,

WPI; 1998-480938/41.

active inhibiting cell nucleic acids, Integrin inhibitors including antibodies, proteins, saccharide(s), capable of binding to integrin(s) as ingredient in remedies - for treating hepatitis, by adhesion

Example 3; Page 16; 35pp; Japanese.

The present sequence is used in the course of the invention. The specification describes Hepatitis drugs which contain integrin inhibitors as the active ingredient. These integrin inhibitors include antibodies, proteins, polypeptides, peptides, nucleic acids, saccharides, and their derivatives. They also include low molecular weight compounds capable of binding to integrins (e.g. alpha chain type with alpha 1, particularly anti-VLA-4 antibody, VLA-4 inhibiting peptides and low molecular weight VLA-4 inhibiting compounds. The products can be used

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as very late antigen-4 (VLA-4) antagonists to treat diseases mediated by cell adhesion. (I) has antiasthmatic, antiallergic, antinflammatory, neuroprotective and antiarteriosclerotic activities. (I) are used to prevent the action of VLA-4 in prevention and treatment of diseases mediated by cell adhesion selected from asthma, allergic rhinitis, multiple sclerosis, atherosclerosis and inflammatory bowel disease. The present sequence represents a synthetic CS-1 peptide which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Very late antigen-4; VLA-4; cell adhesion inhibitor; CD49d/CD29; alpha4/beta7 integrin; cyclic amidine derivative, rhinitis; asthma; multiple sclerosis; atherosclerosis; bowel disease; inflammation; nephritis; AIDS-related dementia; acquired immunodeficiency syndrome; diabetes; conjunctivitis; Alzheimer s disease; aortic stenosis; myeloma; contact dermal hypersensitivit; ulcerative colitis; Crohn's disease; lung disease; cancer; viral infection; meningitis; pulmonary fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes heterocyclic amides (I) which are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of new and known heterocyclic amides as VLA-4 antagonists to treat and prevent disorders mediated by cell adhesion e.g. asthma, allergic rhinitis, multiple sclerosis, atherosclerosis and inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myocarditis; organ transplantation; psoriasis; restenosis; retinitis;
arthritis; stroke; tumour metastasis; uveititis; vascular occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Very late antigen-4 (VLA-4) dependent adhesion related peptide, CS-1.
                                                                                                        VLA-4 antagonist, antiasthmatic; antiallergic; antiinflammatory; neuroprotective; antiarteriosclerotic; asthma; allergic rhinitis; multiple sclerosis; atherosclerosis; inflammatory bowel disease.
                                                                                            Heterocyclic amide; cell adhesion inhibitor; very late antigen-4;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Chang LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Doherty G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU77526 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                      14-AUG-2000; 2000WO-US22115.
                                                                                                                                                                                                                                                                                                                                         99US-0149042.
                                                                                                                                                                                                                                                                                                                                                                                                                    Delaszlo SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC.
                                                      Synthetic CS-1 peptide
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                                                                                                                                                                                                                                                                                                                                         16-AUG-1999;
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                   16-MAY-2001
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                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are cyclised via disulphide or amide bonds. The peptides are very late antigen-4 (VLA-4) adhesion inhibitors. They are useful for treating inflammation, especially allergic inflammation and hepatitis, autoimmune disease, rejection reactions following organ transplants, type I diabetes, Crohn's disease, post-surgical restenosis and arteriosclerosis. The present sequence is used in the course of
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclic hexapeptide; very late antigen-4; VLA-4; adhesion inhibitor; inflammation; allergic inflammation; hepatitis; autoimmune disease; rejection reaction; organ transplant; type I diabetes; Crohn's disease; post-surgical restenosis; arteriosclerosis.
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                                                                          19; Length 13;
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                                                                                                             0; Indels
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                                                                                                             Mismatches
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                                                                          100.0%; Score 23; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB70683 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                  AAY22632 standard, peptide, 13 AA
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Matches 5; Conservative
                                                                                                               Conservative
for treating hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID 57 of WO9925731
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                                                      Query Match
Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-370745/31
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                                       13 AA;
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EILDV 10
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                                                                                                                                                                                                                                                                                                                      AAY22632;
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                                       Sequence
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AAB70683 ID AAB7 XX AC AAB7

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This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaJ heat shock protein (hsp) in modulating an immunome response in a subject. The peptides of the invention may have immunomedulatory, cytostatic, antinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The immunogenic peptide is useful for modulating (i.e. augmenting/inducing or reducing/inhibiting) an immune response in a subject having an immunological disorder (e.g. autoimmune disease such as arthritis or articular juvenile idiopathic arthritis), an infectious disease, an inflammatory bowel disease or cancer. The immunogenic peptide of the invention is also useful for modulating immunogenic peptide of the invention is also useful for modulating immunogenic peptide of the invention is also useful in methods in mammals, e.g. cat, dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In general, the peptide is useful in methods involving mucosal colerisation, DNA vaccination, anergy induction or active immunisation. The present sequence represents a human heat shock protein immunogenic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                        treating immunological disorder in subjects such as humans, e.g.
autoimmune disease (e.g. arthritis), infectious disease, inflammatory
                                                                                                                                                                                                                                                                                                                                                                                New immunomodulatory peptides from heat shock proteins, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 23; Length 15; 100.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                                      Prakken BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triazine; polyethylene glycol; agglutination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                      Carson DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR29632 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 56; 84pp; English.
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                                                                                                                     31-OCT-2001; 2001WO-US45344..
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                                                                                                                                                                   01-NOV-2000; 2000US-245181P.
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nes 5; Conservative
                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       bowel disease or cancer
                                                                                                                                                                                                                                                                                      Albani S,
                                                                                                                                                                                                                                                                                                                               WPI; 2002-489999/52.
                                                                                                                                                                                                                                     (MART/) MARTINI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 AA;
                        WO200236611-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ഗ
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                                                                      10-MAY-2002
                                                                                                                                                                                                                                                                                      Martini A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S EILDV
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Matches
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    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes novel substituted cyclic amidine derivatives (I) are useful for the prevention or treatment of disease or disorders mediated by cell adhesion in a mammal e.g. asthma, allergic rhinitis, multiple sclerosis, atherosclerosis, inflammatory bowel disease or inflammation e.g. acute respiratory distress syndrome (ARDS), ALDS-related dementia, allergic conjunctivitis, Alzheimer's disease, cortic stenosis, autologous bone marrow transplantation, certain types of toxic and immune based nephritis, contact dermal hypersensitivity, ulcerative colitis, Crohn's disease, inflammatory lung disease, inflammatory sequelae of viral infections, meningitis, multiple myeloma, myocarditis, organ transplantation, psoriaais, pulmonary fibrosis, restenosis, retinitis, rheumatoid arthritis, septic arthritis, stroke, cancer, tumour metastasis, uvelitis, type I diabetes and vascular occlusion following angioplasty. The compound inhibits cell adhesion processes including cell activation, migration, proliferation and differentiation. This sequence represents the CS-I peptide used to study the inhibition of very late antigen-4 (VLA-4, CD49d/CD29 or alpha4/beta7 integrin) dependent adhesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New substituted cyclic amidine derivatives for the prevention or treatment of disease mediated by cell adhesion in a mammal e.g. asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 16; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human HSJI immunogenic peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                                Shah S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                       21-MAY-2001; 2001US-0862194.
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Best Local Similarity 100."
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Hagmann WK, Doherty GA,
                                                                                                                                                                                                                                                                                 (HAGM/) HAGMANN W K.
(DOHE/) DOHERTY G A.
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-215831/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AA;
                                                                                          US2002010199-A1.
                                                                                                                                                                                                                                                                                                                               (SHAH/) SHAH S.
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angioplasty
                                              Synthetic.
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The invention relates to a composition comprising an integrin/adhesion antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are based on laminin or saw-scaled viper echistatin and target integrin, selectin or vinculin. Also included are compounds of formula (Ia) and their multimers (\chi^2)_{-} a +F^1-(\chi^2)_{-} b where,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition comprising integrin or adhesion antagonistic peptide and vehicle, useful for treating or preventing platelet aggregation, has a longer half-life than free peptide
                                                                                                                                                                                                                                                                                         antiinflammatory; immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper; echistatin; integrin; selectin; vinculin; platelet aggregation; angiogenesis; tumour; inflammation; autoimmune disease; rheumatoid arthritis; osteoporosis.
                                               13; Length 16,
                                                                     Indels
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                                                                                                                                                                                                                                                                              IgG Fc; anticoagulant; thrombolytic; cytostatic;
                                              DB
53;
inhibitors or drugs for treating neuropathy
                                                                     Mismatches
                                              Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC
                                                                                                                                                                              AAU81181 standard; Peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 21; 68pp; English
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                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001; 2001WO-US13069.
                                                                                                                                                                                                                                                      Laminin-related peptide #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-198919P. 03-MAY-2000; 2000US-201394P.
                                                                                                                                                                                                                              (first entry)
                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-062025/08.
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                                              Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 = Fc domain;
                       16 AA;
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                                                                                            EILDV
                                                                                                                  EILDV
                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                       AAU81181;
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                       Sequence
                                                                                                                                                         68
                                                                                                                                                                   AAU81181
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                                                                                                                                                   One of 1 or 2 of these chains are attached via the N- or C-terminal to a 2,46-trisubstituted s-triazine ring, where one substitution is a polyethylene glycol chain [CH3(OCH2CH2)n-O- (in=1-150)] and the other is either another, same, polyechylene glycol chain, or another, same, peptide chain. These PEG derivates or their salts are useful as animal cell adhesion inhibitors, or as platelet agglutination or adhesion inhibitors. They may also be used as carcinoma metastasis inhibitors, wound healing drugs and immunoregulators.
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This peptide deriv. inhibits adhesion of animal cells, partic platelet aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastasis inhibitor; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
                                                                                                                                                                                                                                                                                                                  ö
                                                                               New peptide(s) contg. PEG derivs. - are cell adhesion and platelet adhesion inhibitors, useful as carcinoma metastasis inhibitors, immuno-regulators and for wound healing
                                                                                                                                                                                                                                                                                          DB 13; Length 16;
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       platelet aggregation; cell adhesion; cancer wound healing; immune inhibitor; neuropathy
                                                                                                                                                                                                                                                                                                   Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                         100.0%; Score 23; 100.0%; Pred. No.
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                                                                                                                             Disclosure; Page 3; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Platelet aggregation inhibitor #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR29104 standard; peptide; 16 AA.
                                 (FUJF ) FUJI PHOTO FILM CO LTD
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            90JP-0316441.
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Best Local Similarity 100.
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                                                         WPI; 1992-274053/33
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                                                                                                                                                                                                                                                                  16 AA;
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           21-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelet
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                                                                                                                         EILDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a f = 0 or 1, provided at least one of a and b = 1, a nucleic acid that encodes (1a), an expression vector containing the nucleic acid, host cells containing the vector, producing a pharmaceutically active compound (B) by covalently linking at least one FC domain to at least one amino acid sequence of a selected randomized (1) and any of sax laminin-related peptides (1b). The compositions are used prophylactically and therapeutically in the same way as (1), e.g. to inhibit platelet aggregation or angiogenesis (tumours), or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integrin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a composition comprising an integrin/adhesion antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are based on laminin or saw-scaled viper echistatin and target integrin selectin or vinculin. Also included are compounds of formula (Ia) and their multimers (x^2)_a - F^2 - (x^2)_b where;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising integrin or adhesion antagonistic peptide and vehicle, useful for treating or preventing platelet aggregation, has a longer half-life than free peptide
                                                                                 Gaps
                                                                                                                                                                                                                                                    IgG Fc; anticoagulant; thrombolytic; cytostatic; antagonist; antiinflammatory; immunosuppressive; osteopathic; antagonist; laminn; saw-scaled viper; echietatin; inceprin; selectin; vinculin; platelet aggregation; anglogenesis; tumour; inflammation; autoimmune disease; rheumatoid arthritis; osteoporosis.
  the half-life (free
vehicle (especially Fc domain) to (I) increases the half-life (frare normally degraded very quickly in vivo). The present sequence is an antagonist peptide of the invention.
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                                                            Length 19;
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                                                           100.0%; Score 23; 100.0%; Pred. No.
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03-MAY-2000; 2000US-201394P.
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                                                                                                                                                                                                                                     Laminin-related peptide #15
                                                                                                                                                                                                                 (first entry)
                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-062025/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC
                                         19 AA;
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                                                                                                     1 EILDV
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                                                                                                                                                                                             AAU81184;
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                                                                                                                                                    RESULT 69
AAU81184
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inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and many different forms of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fr domain) to (I) increases the half-life (free (I) are normally degraded very quickly in vivo). The present sequence is an antagonist peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising integrin or adhesion antagonistic peptide vehicle, useful for treating or preventing platelet aggregation, longer half-life than free peptide
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                                                                                                                                                                                                                                                                                         23; Length 19;
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                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IgG Fc; anticoagulant; thrombolytic; cytostatic;
                                                                                                                                                                                                                                                                                     DB
64;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                         Score 23;
Pred. No.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laminin-related peptide #16.
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Best Local Similarity 100.
Matches 5; Conservative
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AAR30901
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used prophylactically and therapeutically in the same way as (I), e.g. to inhibit platelet aggregation or angiogenesis (tumours), or to treat inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and different forms of osteoporosis, also for diagnosis. Attaching the vehicle (sepecially FC domain) to (I) increases the half-life (free (I) are normally degraded very quickly in vivo). The present sequence is an antagonist peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The peptide is an example of a cell adhesion polypeptide contg. the amino sequence X-Asp-Y-(A)n-Phe, where X and Y = Ala, Leu, Ile or Val. A= any amino acid and n= 3-10. At least a subsequence of the polypeptide is adherent for MoLT-4 human lymphoblastic leukaemia, A375-SM human metastatic melanoma or H1080 human fibrosarcoma cells. The call adhesion peptides are used to modify or control the adhesion peptides are used to modify or control the conditions such as rheumatoid arthritis, asthma, sepsis, graft rejection, inflammatory bowel disease, reperfusion of cardiac tissue after myocardial infarction, and coagulatory disorders. They are selective antagonists of cell adhesion, e.g. they promote adhesion of the speccified cells but inhibit adhesion to the natural adhesion
                                                                                                                                                         Gaps
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/note= "LDV region followed by Phe at position 17."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cell adhesion (poly)peptide(s) modifying cell adhesive
properties - useful in treating inflammatory conditions e.g.
rheumatoid arthritis, asthma, inflammatory bowel disease, sepsis,
                                                                                                                                                         ö
                                                                                                                             Query Match

100.0%; Score 23; DB 23; Length 19;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                     AAR26821 standard; peptide; 20 AA.
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91GB-0002818.
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                                                                                                                                                                                                                                                                                                                                               Cell adhesion polypeptide
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                                                                                                       19 AA;
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                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLT-4; human; lymphoblastic leukaemia; A375-SM; metastatic; melanoma; H1080; fibrosarcoma; LDV; LDL; IDA; inflammatory disease; rheumatoid arthritis; asthma; sepsis; graft rejection; reperfusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cell adhesion (poly)peptide(s) modifying cell adhesive properties - useful in treating inflammatory conditions e.g. rheumatoid arthritis, asthma, inflammatory bowel disease, sepsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                  Score 23; DB 13; Length 20;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IndelB
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                                                                                                                                                                                        0; Mismatches
protein contg. the adhesive sequence. See also AAR26822-30 and AAR30887-903.
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See also AAR26821-30 and AAR30887-903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 11; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR30901 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell adhesion polypeptide CS12.
                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92WO-GB00226.
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91GB-0002818.
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                                                                                                                                                                                        5; Conservative
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Matches 5, Conserv
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Matches S; Conserv
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                                                                               20 AA;
                                                                                                                                                                                                                                              1 EILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-1991;
                                                                                                                                                                                                                                                                              4 BILDV
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                                                                                  Sequence
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                                                                                                                                     Query Match
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RESULT 73

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The present sequence represents an alpha4 integrins targeting sequence, which is used in an example from the present invention. The present invention describes a chimeric adenovirus fibre protein (AFP) containing a constrained non-native amino acid sequence. The non-native amino acid sequence allows the chimeric fibre (or a vector comprising the chimeric fibre) to more efficiently bind to and enter cells. The products can be used for gene therapy, for treating cancer, e.g. melanoma, glioma and lung cancers as well as genetic disorders, e.g. cystic fibrosis, haemophilia and muscular dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g. prevent restenosis following angioplasty or to promote angiogenesis to reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
                                                                          Chimeric; adenovirus; fiber protein; binding; targeting; coat protein; constrained peptide motif; gene therapy; cancer; heart disease; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic, conjugated polypeptide; herpes simplex virus; HSV; ICP4; immunomodulatory; T cell, immunogen; vaccine; ICP27; glycoprotein B; ribonucleotide reductase; ICP34, 5; glycoprotein B; glycoprotein F; immune response; genetic immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric adenovirus fibre proteins - containing non-native amino acid sequence to provide for binding and entry into cells, especially for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23; DB 19; Length 21; Pred. No. 71;
                                          Alpha4 integrins targeting sequence SEQ ID NO:57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kovesdi I, Roelvink PW, Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 57; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY13421 standard; peptide; 23 AA.
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ilarity 100.0%;
Conservative 0;
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  29-JUL-1998 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             (GENV-) GENVEC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AA;
                                                                                                                                                               Synthetic.
Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                  21-AUG-1996;
                                                                                                                                                                                                                                                                                                            21-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a specifically claimed non-native amino acid sequence from a chimeric adenovirus fibre protein (AFP) of the present invention. The non-native amino acid sequence allows the chimeric fibre (or a vector comprising the chimeric fibre) to more efficiently bind to and enter cells. The products can be used for gene therapy. For trearing cancer, e.g. melanoma, glioma and lung cancers as well as genetic disorders, e.g. cystic fibrosis, haemophilia and muscular dystrophy as well as pathogenic infections, e.g. HIV, truberculosis and hepatitis and also for heart disease, to e.g. prevent restenosis following angioplasty or to promote angiogenesis to reperfuse necrotic tissue, and in autolimmune disorders, e.g. Crohn's disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                 Chimeric; adenovirus; fiber protein; binding; targeting; coat protein; constrained peptide motif; gene therapy; cancer; heart disease; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                   Chimeric adenovirus fiber protein non-native amino acid sequence 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric adenovirus fibre proteins - containing non-native amino acid sequence to provide for binding and entry into cells, especially for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wickham IJ;
                                                                                                                                          AAW56047 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US14719.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I, Roelvink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-169169/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENV-) GENVEC INC.
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                Mastadenovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1996;
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                     EILDV
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                                                                                                                                                                                  AAW56047;
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The invention provides immunogenic conjugated polypeptides which comprise a herpes simplex virus peptide (HSV) linked to an immunomodulatory peptide and which promote binding to T cells. The novel immunogenic conjugated polypeptides are effective as an immunogen in a vaccine for treatment or prevention of infection by HSV and are represented by the formula Pl-x-P2 or P2-x-P1; where Pl = a HSV specific antigenic peptide form a protein of HSV type lo or type 2, selected from ICP27, glycoprotein E, ribonucleotide reductase, ICP4, ICP34-S, glycoprotein E and immunomodulatory peptide which is a portion of an immunoprotein P; P2 = an immunomodulatory peptide which is a portion of an immunoprotein bond or a class of subclass of T cells and which directs a predominantly TH1 type, immune response to the peptide CP1; and x = a covalent bond or a clasvable or non-clasvable peptide CP1; and x = a covalent bond or a clasvable or non-clasvable peptide CP1; and x = a covalent bond or a clasvable or non-clasvable peptide CP1; and x = a covalent bond or a clasvable or non-clasvable peptide CP1; and x = a covalent bond or a clasvable or non-clasvable peptide CP1; and x = a covalent bond filling HSV infected cells. They can be used for the treatment or prevention of HSV infection. In addition, DNA encoding the polypeptide and detecting a reaction between the T cells and the colls and the polypeptide. CP1 polypeptide or latent, in an cindividual by HSV by mixing T cells from the individual with the polypeptide.
                                                                                                                                                                                                                                                                                                                                                   New immunogenic conjugated polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 33; 69pp; English.
                                                                                                                                                                                  CEL-SCI CORP.
UNIV NORTHEASTERN OHIO.
                                                                                                                                                                                                                                                        Rosenthal KS, Zimmerman DH;
                                                                                          98WO-US20681.
                                                                                                                                      97US-0060422
                                                                                                                                                                                                                                                                                                    WPI; 1999-312418/26
WO9916710-A1.
                                                                                                                                   30-SEP-1997;
                                                                                          29-SEP-1998;
                                           08-APR-1999.
                                                                                                                                                                                  (CELS-)
                                                                                                                                                                                                          (UYNE-)
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; 0 100.0%; Score 23; DB 20; Length 23; llarity 100.0%; Pred. No. 78; Conservative 0; Mismatches 0; Indels Best Local Similarity Matches 5; Conserv 23 AA; Sequence Query Match

EILDV 9 1 EILDV 5 셤 ઠ

Search completed: February 8, 2003, 10:23:45 Job time : 38 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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8, 2003, 10:24:48; Search time 11 Seconds (without alignments) 10.077 Million cell updates/sec OM protein - protein search, using sw model February Run on:

US-09-251-073A-16 23 Perfect score:

1 EILDV 5 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

129505 seqs, 22169297 residues Searched:

Total number of hits satisfying chosen parameters:

28

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOB NEW FUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 6, Appli	Sequence 3, Appli	Sequence 80, Appl	Sequence 5, Appli	Sequence 56, Appl	Sequence 14, Appl	Sequence 95, Appl	~	٠,		Sequence 59, Appl	Sequence 119, App	Sequence 11, Appl	Sequence 76, Appl	Sequence 900, App		Sequence 4085, Ap	Sequence 10394, A	Semence 13921. A
-	QI	US-10-086-217-6	US-09-320-907B-3	US-09-969-192-80	US-10-086-217-5	US-09-969-192-56	US-10-137-435-14	US-09-840-277-95	US-09-840-277-96	US-09-840-277-133	US-09-969-192-57	US-09-969-192-59	US-09-840-277-119	US-09-010-714-11	US-09-969-192-76	US-09-925-301-900	US-09-738-626-5384	US-09-738-626-4085	US-09-815-242-10394	US-09-815-242-13921
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de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Sequence 14, Appl Sequence 700, App Sequence 6113, Ap Sequence 492, App Sequence 6119, Ap Sequence 13699, A Sequence 23, Appl Sequence 9, Appl Sequence 5, Appl
US-10-029-654-14 US-09-925-302-700 US-09-738-626-6313 US-09-738-626-6019 US-09-738-626-6019 US-09-815-242-13699 US-10-145-014-23 US-08-910-386A-9 US-08-910-386A-5
117 110 110 110 110
394 4117 560 736 737 737 737 737 737
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ALIGNMENTS

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Sequence 6, Application US/10086217

Sequence 6, Application US/10086217

Patent No. US2002015998A1

GENERAL INFORMATION:

APPLICANT: WUNDY, GREGORY R.

APPLICANT: WONEDA, TOSHIYUKI

TITLE OF INVENTION: METHODS OF TREATING MULTIPLE MYELOMA AND

TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN

TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN

TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN

TITLE OF INVENTION: MYBER: US/10/086,217

CURRENT PILING DATE: 2001-08-31

PRIOR PILING DATE: 2001-08-31

PRIOR PILING DATE: 1998-09-13

PRIOR PILING DATE: 1998-09-14

NUMBER OF SEQ ID NOS: 8

SOFTWARE PATENTION VOLUBER: 60/100,182

PRIOR FILING DATE: 1998-09-14

NUMBER OF SEQ ID NOS: 8

SOFTWARE PATENTING DATE: 1998-09-14

NUMBER OF SEQ ID NOS: 8

LENGTH: 5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-086-217-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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Sequence 3, Application US/09320907B

Sequence 3, Application US/09320907B

SUBJECT INFORMATION:

APPLICANT: GINSBERG, MARK H.

APPLICANT: GINSBERG, MARK H.

TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF

TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS

FILE REPERBNCE: SRI-0006

CURRENT FILING DATE: 1999-05-27

PRIOR APPLICATION NUMBER: 09/187,236

PRIOR APPLICATION NUMBER: 09/187,236

PRIOR FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3: SEQ ID NOS: 25

LENGTH: 5 US-09-320-907B-3

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RESULT 5
US-09-969-192-56
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                                                                                                                                     Gaps
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                   ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-320-907B-3
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COMPUTER: ISE FIGURE ASSETS.

COMPUTER: ISE FIGURE ASSETS.

COMPUTER: ISE FIGURE ASSETS.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/969,192

FILING DATE: 01-0ct-2001

PRIOR APPLICATION NUMBER: US 9-455061

FILING DATE: 06-DEC-199

APPLICATION NUMBER: US 9-130225

FILING DATE: 06-AUG-1996

APPLICATION NUMBER: US 9-130225

FILING DATE: 21-AUG-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
                                                                                            100.0%; Score 23; DB 9; Length 5; 100.0%; Pred. No. 1.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    Sequence 80, Application US/09969192
Patent No. US20020151027A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
ROELVINK, PETRUS W.
KOVESDI, IMRE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 10;
100.0%; Pred. No. 1.1e+05;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 213564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
ORGANISM: Artificial Sequence
                                                                          Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                        1 EILDV 5
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RESULT 4 US-10-086-217-5

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Sequence 5, Application US/10086217
PREAL INFORMATION:
APPLICANT: WINDY, GREGORY R.
APPLICANT: WINDY, GREGORY R.
TITLE OF INVERTION: MITCHA-INDUCED BORR RESORPTION USING INTEGRIN TITLE OF INVERTION: MITCHA-INDUCED BORR RESORPTION USING INTEGRIN TITLE OF INVERTION: MITCHA-INDUCED BORR RESORPTION USING INTEGRIN TITLE OF INVERTION: MATCHA-INDUCED BORR RESORPTION USING INTEGRIN TITLE OF INVERTION: MATCHA-INDUCED BORR RESORPTION USING INTEGRIN TITLE OF INVERTION: MATCHA-INDUCED BORR RESORPTION USING INTEGRIN USING APPLICATION WARRES: 09/40-540
PRIOR FILMS DATE: 2001-08-13
PRIOR PRIOR FILMS DATE: 1999-09-13
PRIOR FILMS DATE: 1999-09-13
PRIOR FILMS DATE: 1999-09-13
PRIOR FILMS DATE: 1999-09-13
PRIOR FILMS DATE: 1999-09-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 23; DB 9; Length 19; Best Local Similarity 100.0%; Pred. No. 7.6; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                           APPLICANT: KORNO, TADAHIKO
APPLICANT: KORNO, TADAHIKO
APPLICANT: LACEY, DAVID LEE
APPLICANT: LACEY, DAVID LEE
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
FILE REFERENCE: A-688A
CURRENT APPLICATION UNMBER: US/09/840,277
CURRENT APPLICATION NUMBER: 60/198,919
PRIOR FILING DATE: 2000-04-21
PRIOR FILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PATENTIN VENSION 3.1
SEQ ID NO 95
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS FILE REFERENCE: A-688A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURENT APPLICATION NUMBER: US/09/840,277
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/201,394
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin vergion 3.1
SEQ ID NO 96
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Laminin related peptide
US-09-840-277-95
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; OTHER INFORMATION: Laminin related peptide
US-09-840-277-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 96, Application US/09840277
Patent No. US20020168363A1
GENERAL INFORMATION:
Application US/09840277
320020168363A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FEIGE, ULRICH
APPLICANT: KOHNO, TADAHIKO
APPLICANT: LACEY, DAVID LEE
APPLICANT: BOONE, THOMAS CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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US-09-840-277-133
Sequence 95, Ap
Patent No. US20
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/137,435
FILING DATE: 03-May-2002
APPLICATION DATA:
APPLICATION NUMBER: US/09/424,656|
FILING DATE: -OURANOWS 9711115.7
FILING DATE: 29-MAY-1997
                                                                                                                                                                                                                                                                              Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 23; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 5; Conservative 0; Mismatches 0; Indels
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100.0%; Score 23; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
STREET: c/o Institute of Child Health,
30 Guildford Street
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                        REFERENCE/DOCKET NUMBER: 213564
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                   STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-969-192-56
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Hart, Stephen Lewis
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: G.B.
ZIP: WOLN 1EH
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                    LENGTH: 8 amino acids
TYPE: amino acid
                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: London
                                                                                                                                                                                                                                                                                                                                                                1 EILDV 5
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                                                                                                                                                    ; Score 23; DB 10; Length 21;
; Pred. No. 8.5;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WICKHAM, THOMAS J.
ROBLVINK, PETRUS W.
KOVEGIJ, INRE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UMBER: US/09/969,192
FILING DATE: 01-Oct-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONSTRAINED PEPTIDE MOTIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 23, DB 10;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 9-455061
FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
                                   TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-969-192-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 59: US-09-969-192-59
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59, Application US/09969192
Patent No. US20020151027A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      100.0%;
                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 59
SEQUENCE CHARACTERISTICS
                                                                                                                                                    Ouery Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                         1 EILDV 5
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US-09-840-277-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 57, Application US/09969192
Patent No. US20020151027A1
GENERAL INFORMATION: THOMAS J.
APPLICANT: WICKHAM, THOMAS J.
ROBLVINK, PETRUS W.
KOVESDI, IMRE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF CONSTRAINED PEPTIDE MOTIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                             TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                      TILE REFERENCE: A-688A
CURRENT APPLICATION NUMBER: US/09/840,277
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR PILING DATE: 2000-04-21
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-05-03
SOFTWARE: PARENTIN VERSION 3.1
SEQ ID NO 133
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-0ct-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: Laminin related peptide
US-09-840-277-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 9-455061
FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 213564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
                                                          KOHNO, TADAHIKO
LACEY, DAVID LEE
BOONE, THOMAS CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 5; Conservative
US20020168363A1
                                          ULRICH
                                        APPLICANT: FEIGE,
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US-US-92-51-5101-90

Patent No. US20020052308A1

GENERAL INPORMATION:

GENERAL INPORMATION:

FILE REFERENCE: PA106

CURRENT PAPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-0

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 900

LENGTH: 152

TYPE PRIOR

GENERAL: Homo sapiens

US-09-925-301-900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%; Score 23; DB 10; Length 152; Similarity 100.0%; Pred. No. 74; 5; Conservative 0; Mismatches 0: Indels (
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-Oct-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                      NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: 111inois
  CONSTRAINED PEPTIDE MOTIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 23; DB 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 9-455061
FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-969-192-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
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APPLICANT: Furcht, Leo T.
APPLICANT: Furcht, Leo T.
APPLICANT: Idea, Joji
TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
TITLE OF INVENTION: ACTIVITY
FILE REPRENCE: 600.3320301
CURRENT APPLICATION NUMBER: US/09/010,714
CURRENT FILING DATE: 1998-01-22
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 11
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Patent No. US20020151027A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
ROGLLVINK, PETRUS W.
KOVESDI, IMRE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
                                                                                                                                              TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
FILE REFERENCE: A-688A
CURRENT APPLICATION WUMBER: US/09/840,277
CURRENT APPLICATION NUMBER: 60/198,919
PRIOR APPLICATION NUMBER: 60/201,394
PRIOR RILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/201,394
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin version 3.1
SEQ ID NO 119
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Laminin related peptide US-09-840-277-119
Sequence 119, Application US/09840277 Patent No. US20020168363A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09010714
Patent No. US20020012942A1
GENERAL INFORMATION:
                                                               APPLICANT: FEIGE, ULRICH
APPLICANT: KOHNO, TADAHIKO
APPLICANT: LACEY, DAVID LEE
APPLICANT: BOONE, THOMAS CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-11
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US-09-969-192-76
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US-09-010-714-11
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Length 366;
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APPLICANT: Obligan, Kari L.

APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.

APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
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APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANTON NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10394, Application US/09815242
Patent No. US20020061569A1
GRNERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Chlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13921, Application US/09815242
Patent No. US20020061569A1
GENERAL-INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                             TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4085
                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 5; Conservative
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286 EILDV 290
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US-09-815-242-10394
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US-09-815-242-13921
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SEQ ID NO 4085
LENGTH: 344
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100.0%; Score 23; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTACE.

TITLE OF INVENTACE.

CURRENT APPLICATION NUMBER: US/09/738,626

CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR PILING DATE: 1999-12-16

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARR: PATENTIN Ver: 3.0

SEQ ID NO 5384
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APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENGH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
FILE REFERENCE: 249-125
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR PELING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                 RESULT 16
US-09-738-626-5384
Sequence 5384, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-738-626-4085; Sequence 4085, Application US/09738626; Sequence 4085, Application US/09738626; Dublication No. US20020197605A1; GENERAL INFORMATION: APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, MASATO
APPLICANT: OSENOH, MASATO
APPLICANT: OSENOH, MASATO
APPLICANT: OSENOH, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 EILDV 122
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12 EILDV 16
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Gaps

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h 100.0%; Score 23; DB 10; Length 417; Similarity 100.0%; Pred. No. 2.2e+02; 5; Conservative 0; Mismatches 0; Indels (
               GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT APPLICATION NUMBER: DCT/US00/05918

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 700-03-08

LENGTH: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFFLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEO ID NOS: 7059
SOFTWARE: PATENTIN VEY: 3.0
SEO ID NO 6313
LENGTH: 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6313, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6313
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US-09-841-132-492
; Sequence 492, Application US/09841132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication NC. 1001.
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI
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TATEISHI, NAOKO
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IKEDA, MASATO
OZAKI, AKIO
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Best Local Similarity 100.
    Patent No. US20020044941A1
                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-925-302-700
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Fatent No. US20020150958A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bechringer Ingelheim Pharma KG
TITLE OF INVENTION: Methods for identifying substances for treating
TITLE OF INVENTION: inflammatory conditions
FILE REPERENCE: 1/178
CURRENT APPLICATION NUMBER: US/10/029,654
CURRENT FILING DATE: 2001-12-21
FRIOR APPLICATION NUMBER: US 60/257,878
FRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
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           APPLICANT: Cart. Grant J.
APPLICANT: Cart. Grant J.
APPLICANT: Cart. Grant J.
APPLICANT: Yamamocto, Robert T.
APPLICANT: Yamamocto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PESESEQ FOR Windows Version 4.0
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US-09-925-302-700
; Sequence 700, Application US/09925302
Trawick, John D.
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Best Local Similarity 100.
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US-09-815-242-13921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 5; Conservative
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US-10-029-654-14
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100.0%; Score 23; DB 9; Length 418; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels
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535 EILDV 539
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| Patent No. US20020061848A1
| GENERAL INPORMATION:
| APPLICANT: Bhairy | Aliay | APPLICANT: Skaiky, Yasir A.W. | APPLICANT: Skaiky, Yasir A.W. | APPLICANT: Probet, Peter | TILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND ITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION | TILLE OF INVENTION UNMERR. US/09/841,132 | CURRENT APPLICATION NUMBER: US/09/841,132 | CURRENT FILING DATE: 2001-04-23 | NUMBER OF SEQ ID NOS: 599 | SOFTWARE: FastSEQ for Windows Version 3.0/4.0 | SEQ ID NO 492 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE0 | LEGTH: SE
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100.0%; Score 23; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
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ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6019
LENGTH: 706
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COCATION: (1)...(560)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-841-132-492
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
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ANDO, SEIKO
HAYASHI, MIKIRO
CCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Chlamydia pneumoniae
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US-09-738-626-6019
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ORGANISM:
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GENERAL INFORMATION
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APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
APPLICANT: Hibbert, Scot
APPLICANT: Richter, Tocot
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resisitance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STARE: California
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100.0%; Pred. No. 4.70+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                            0; Indels
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MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/910,386A

FILING DATE: 13-AUG-1997

CLASSIFICATION NUMBER: US/08/910,386A

FILING DATE: 13-AUG-1997

ATTORNEY/AGBNT INFORMATION:

NAMME: Bastian, Kevin L.

REGISTRATION NUMBER: 03.070-058950US

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 813 amino acids

TYPE: amino acid

TOPOLOGY: Inear

MOLECULE TYPE: protein

US-08-910-386A-9
                                                                                                                                                          Query Match
100.0%; Score 23; DB 9; I
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       US-08-910-386A-9
Sequence 9, Application US/08910386A
Patent No. US20020092041A1
GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-10-145-014-23
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Sequence 5, Application US/08910386A Patent No. US20020092041A1

RESULT 28 US-08-910-386A-5

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US-08-817-154-2

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US-08-700-515-3
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Sequence 3, Application US/08109106

Sequence 3, Application US/08109106

SEGUENCE 3, Application US/08109106

STATIA OF THORNARD ALLIES ALLIELS Antibody

WUMBER OF SEGUENCES: Life in Antibody

CORRESPONDENCE ALDRESS:

ADDRESSES: Wenderoth, Lind & Ponack

STREET: 005 Fifteenth Street, N.W., #700

CORPUTES: 180 Fifteenth Street, N.W., #700

CORPUTES: 180 Fifteenth Street, N.W., #700

CORPUTES: 180 Fifteenth Street, N.W., #700

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Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,162A
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Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
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FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KIJYK, JOhn Jr.
REGISTRATION NUMBER: 30763
REPERENCE/DOCKET NUMBER: 61306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEPAX: (312) 616-5600
TELEPAX: (312) 616-5700
TELEPAX: (312) 616-5700
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                   FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-08-109-106-3
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STRANDEDNESS: single
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MOLECULE TYPE: protein
            TITLE:
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                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTORNEY/AGENT INFORMATION:
NAME: SUNGMEN, 20hn, 5.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 24,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECOMMUNICATION INFORMATION:
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APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Imre
APPLICANT: Brough, Douglas B.
APPLICANT: Brough, Douglas B.
APPLICANT: Bruder, Joseph T.
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windowst
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,515
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CLASSIFICATION: 514
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
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Sequence 3, Application US/08709515
Patent No. 5731190
GENERAL INFORMATION:
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TELEX: 4938023
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 5 amino acids
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TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
NUMBER OF SEQUENCES: 12

OORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                Sequence 3, Application US/08634060
| Sequence 3, Application US/08634060
| Sequence 3, Application US/08634060
| Patent No. 5712130:
| Patent No. 5712130:
| APPLICANT: Wickham, Thomas J.
| APPLICANT: Rowesdi, Imre
| APPLICANT: Rowslin in the APPLICANT: Rowesdi, Imre
| APPLICANT: Rowerlin in the APPLICANT: Rowerlin in the APPLICANT: Rowerlin in the APPLICANT: Rowerlin in the APPLICANT: Rowerlin in the APPLICANT: APPLICANT: APPLICANT: APPLICANT IN THE APPLICANT: APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE APPLICANT IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 1; I
100.0%; Pred. No. 1.9e+05;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
ATTONEY/AGANT INFORMATION:
NAME: KIJYK, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71602
TELEPHONE: (312) 616-5600
TELEPAN: (312) 616-5600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-338-282-10
; Sequence 10, Application US/08338282
; Patent No. 5730978
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-634-060-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: USA
1 EILDV 5
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Gaps
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                                                                                                                                                                                                                                                        APPLICANT: Jeffrey W. Smith
APPLICANT: Jeffrey W. Smith
TITLE OF INVENTION: Integrin Ligand Dissociators
FILE REPERRICE: 02046.0002
CURRENT APPLICATION NUMBER: US/09/146,503
CURRENT FILING DATE: 1998-09-02
EARLIER FILING DATE: 1997-09-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO: 3
LENGTH: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 4; 100.0%; Pred. No. 1.9e+05; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cast.O. ALICANES
APPLICANT: Cuervo, Julio Herman
APPLICANT: Cuervo, Julio Herman
APPLICANT: Lee, Wen-Cherng
APPLICANT: Lee, Wen-Cherng
APPLICANT: Carter, Mary Beth
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: DISINGER: US/08/983,391
CURRENT FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 96/11570
SRIOR FILING DATE: 1995-07-11
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
LENGTH: 5
                                                                                                                                                                                     Sequence 3, Application US/09146503
Patent No. 6184206
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08983391
Patent No. 6239108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Synthetic
US-09-146-503-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin, Ko-Chung
Adams, Steven P.
Castro, Alfredo C.
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Best Local Similarity 100.(
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08700846

Patent No. 5962311

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
TITLE OF INVENTION: ASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900

CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: 11.
CUNTRY: 10.

ZIP: 60601-6780

COMPUTER READBABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,846
FILING DATE: 21-AUG-1996
CLASSIPICATION: 514
ATTONNEY/AGENT INPORMATION:
NAME: LARCHER, CAROL
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 35243
REFERENCE/DOCKET NUMBER: 36243
RELEFAX: (312) 616-5600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEGENAX: (312) 616-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEGINATION FOR SEQ ID NO: 2:
LEGITH = 10.0 min a cide
LEGITH = 10.0 min a cide
LEGITH = 10.0 min a cide
FILING DATE: 08-SEP-1954
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 73845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-709-515-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/376,372
FILING DATE:
FILING DATE:
FLING DATE:
FRESTENCATION NUMBER: 27,794
ATTORNEY/AGENT INFORMATION:
FRESTENCAPOCKET NUMBER: B180
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPK: 14-8367
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACTERISTICS:
LENGTH: 5 amino acids
worne: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 23; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
APPLICANT: Zimmerman, Craig N
APPLICANT: Hammend, Craig N
APPLICANT: Hammond, Charles E
APPLICANT: Liao, Yu-Sheng
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OF EXQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lin, Ko-chung
APPLICANT: Lin, Ko-chung
APPLICANT: Lin, Ko-chung
APPLICANT: Lew Wen-Cherng
APPLICANT: Castro, Alfredo C.
APPLICANT: Zimmerman, Craig N.
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Singh, Juswinder
ITLE REFERENCE: 10274-023002
CURRENT APPLICATION NUMBER: US/08/875,321
CURRENT APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR PILING DATE: 1995-01-23
NUMBER OF SEQ ID NOS: 5
LENGTH: S
                                                                                                                                                                                                                                                                                                                                                      New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08875321
Patent No. 6376538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                               STATE: New
COUNTRY: Un
ZIP: 10020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTLE OF INVENTION: KODALG US
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
CUNTRY: United States of America
ZIP: 1020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEAPC compatible
COMPUTER: DATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee, Wen-Cherng
Hammond, Charles B
Carter, Mary B
Almquist, Ronald G
VENTION: CELL ADHESION INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               RESUL: 7
US-08-498-237-2
i Sequence 2, Application US/08498237
j Patent No. 6248713
i GENERAL INFORMATION:
i APPLICANT: Lin, Ko-Chung
j APPLICANT: Castro, Alfredo C
APPLICANT: Castro, Alfredo C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08376372
Patent No. 6306840
GENERAL INFORMATION:
APPLICANT: Adams, Steven P
APPLICANT: Lin, Ko-Chung
APPLICANT: Lin, Ko-Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zimmerman, Craig N
Cuervo, Julio H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-498-237-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserva
                                                                                   EILDV 5
                                    EILDV S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
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/note= "3-AMINO-PROPIONIC ACID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COURTEX OF SECULATION OF ADDRESS ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADDRESSES ADD
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,124
FILING DATE: 21-ANG-1996
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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OTHER INFORMATION:
US-08-860-248C-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         circula
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                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EILDV 5
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TITLE OF INVENTION: DOMAINS OF TRANSMEMBRANE RECEPTORS
NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PATENTIN NUMBER: PCT/US95/07542
FILING DATE: 13-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/260,514
FILING DATE: 15-UNN-1995
SPUING DATE: 15-UNN-1995
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERITICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vuery match

Best Local Similarity 100.0%; Pred. No. 1.9e+05; Length 5; Matches 5; Conservative n. Minches
                                                                                                                                              Query Match 100.0%; Score 23; DB 4; Length 5; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 5; Conservative 0; Mismatches 0; Indels
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Patent No. 5846782

GENERAL INFORMATION:

APPLICANT: Rickham, Thomas J.

APPLICANT: Roelvink, Petrus W.

ATTLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSE: Leydig, Voit & Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Ligand sequence recognized by integrin
                                                          , OTHER INFORMATION: Synthetically generated peptide
US-08-875-321-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application PC/TUS9507542
GENERAL INFORMATION:
APPLICANT:
   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 amino acida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
GY: linear
                                                                                                                                                                                                                                                                                                            1 EILDV 5
                                                                                                                                                                                                                                                                    1 EILDV 5
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PCT-US95-07542-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-701-124-80
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Length 7;
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TORRESPONDENCE: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "OTHER"
/note= "6-AMINO-HEXANOIC ACID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 3; I
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                  SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: PLODPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                  COUNTRY: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
"MEDIUM TYPE: Ploppy disk
"MEDIUM TYPE: Ploppy disk
"MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 7
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
ADDRESSEB: Pillsb
STREET: 1100 New
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-860-248C-52
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US-08-860-248C-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0, Indels
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US-08-860-248C-52
Squence 52, Application US/08860248C
Sequence 52, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TILLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIERONECTIN ADHESION INHIBITORS
NUMBER OP SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillabury Madison & Sutro, L.L.D.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "5-AMINO-PENTANOIC ACID
  100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: MS WORD

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION NUMBER: GB 9505905.1
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 mainto acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 US-08-860-248C-51
; Sequence 51, Application US/08860248C
Patent No. 6034056
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 5; Conservative
                         Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: 7 CTHER INFORMATION: 9 CTHER INFORMATION: US-08-860-248C-51
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  Best Local Similarity
Matches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                             1 RILDV 5
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                                                                                                                                                              RESULT 15
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Query Match 100.
Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: 81
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100.0%; Pred. No. 1.9e+05;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 80, Application US/09130225
; Batent No. 6057155
; General INFORMATION:
    APPLICANT: Rochvink, Petrus W.
    APPLICANT: Rochvink, Petrus W.
    APPLICANT: Kovesdi, Imre
    TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
    TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
    NUMBER OF SEQUENCES: 80
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Leydig, Voit & Mayer, Ltd.
    STREET: Two Prudential Plaza - 49th Floor
    CITY: Chicago
    STREET: Illinois
    COUNTRY: USA
    CONFUTER: Illinois
    COMPUTER: Eloppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PATENTIN Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/130,225
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100.0%; Score 23; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           /product= "OTHER"
/note= "8-AMINO-OCTANOIC ACID"
FILING DATE: 24-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR.1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL.1995
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acids
STRANBENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
PRIOR APPLICATION DATA:
PRICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 80:
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LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                             SS: single circular
                                                                                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: peptide
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                     FEATURE:

NAME/KEY: Peptide

LOCATION: 7

OTHER INFORMATION: //

US-08-860-248C-53
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APPLICANT: TSUKADA, YOSHIDISA
APPLICANT: TSUKASA, ATSUSHI,
TITLE OF INVENTION: PEPTIDE-CONTAINING POLYETHYLENE GLYCOL
TITLE OF INVENTION: DERIVATIVES AND APPLICATION THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHTURE, MION, ZINN, MACPEAR AND SEAS
Sequence 80, Application US/09455061

Patent No. 6329190

GENERAL INFORMATION: Thomas J.

APPLICANT: Roelvink, Petrus W.

APPLICANT: Kovedi, Ince

TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Voit & Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 9-130225
FILING DATA: 06-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
ATTONREY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Sughrue, Mion, Zinn, Macpeak and Seas 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 4;
100.0%; Pred. No. 1.9e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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CITY: Washington
STATE: D.C.
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Sequence 7, Application US/08338282
Patent No. 5730978
GENERAL INFORMATION:
APPLICANT: WAYNER, E.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christeensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 23; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                               Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSES: CITIETERIES, O'CORNOI, JOHNSON AND ALGESTES.

CITY: Seattle
STREET: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIOU TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
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COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.24-0779
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                                                                                               Query Match
100.0%; Score 23; DB 1, I
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
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US-08-701-124-56
'Sequence 56, Application US/08701124
'Parent No. 5846782
; GENERAL INFORMATION:
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EILDV PST
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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DESCRIPTION:
            HYPOTHETICAL:
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                           US-08-158-936-1
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Patent No. 5521067
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bone Marrow Cell Adhesion Molecules and
TITLE OF INVENTION: Process for Detecting Adherence Between Cell Adhesion
TITLE OF INVENTION: Molecules and Cells Generally
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: 1
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: Mixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
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COUNTRY: USA
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/780,081
FILING DATE: 19911021
CLASSIFICATION: 530
TELEPHONE: 202-293-7660
TELEFROMICATION INFORMATION:
TELEPHONE: 202-293-7660
TELEFRAX: 202-293-7660
TELEFRAX: 202-293-7660
TELEFRAX: 202-293-7660
TELEFRAX: AMINO ACID
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
STRANDENESS: single
TYPE: AMINO ACID
STRANDENESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUNTRY: Now York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
CURRENT APPLICATION NUMBER: US/08/158,936
FILING DATE: No. 5521067ember 24, 1993 |
FILING DATE: No. 5521067ember 24, 1993 |
FLING DATE: No. 6321067ember 24, 1993 |
FLING DATE: NO. 727 |
REGISTRATION NUMBER: 30,727 |
REGISTRATION NUMBER: 176/60030 |
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 5; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-780-081-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: derived from fibronectin
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US-08-467-580-3
US-08-467-580-3
Sequence 3, Application US/08467580B
Patent No. 6001809
GENERAL INFORMATION:
APPLICANT: Thorsett, Eugene D
APPLICANT: Thorsett, Theodore A
APPLICANT: Pleiss, Michael A
TILE OF INVENTION: Inhibitors of Leukocyte Adhesion
FILE REFERENCE: 123-US-CIP1
CURRENT APPLICATION NUMBER: US/08/467,580B
CURRENT APPLICATION NUMBER: US/08/467,580B
GERLIER APPLICATION NUMBER: 08/273,055
BARLIER FILING DATE: 1994-07-11
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 8
TENDING THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THEORY THE
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Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 23; DB 2; 3
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: ACETYLATION
US-08-467-580-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative 0
                                                                                                             TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                        LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Prudiction CITY: Chicago STATE: Illinois COUNTRY: USA
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NAME/KEY: MOD_RES
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US-09-130-225-56
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Patent No. 5558874
GENERAL INFORMATION:
APPLICANT: Clark, Richard A
APPLICANT: Gailing, Doris
APPLICANT: Gailit, James
TITLE OF INVENTION: EXCOMBINANT FIBRONECTIN-BASED
TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSE: Jackel Fleischmann & Mugel, LLP
STREET: 39 State Street
        APPLICANT: ACCIVING, PETRUS W.
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor CITY: Chicago STATE: Illinois
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 23; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,706
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87653.97R263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716-262-4133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
Wickham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rochester
STATE: New York
COUNTRY: USA
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US-09-025-706-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetically generated protein US-08-983-391-1
  Pred. No. 1.9e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lee, Wen-Cherng
APPLICANT: Hammond, Charles B
APPLICANT: Carrer, Mary B
APPLICANT: Almquist, Ronald G
TITLE OF INVENTION: CELL ADHESION INHIBITORS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carrer, Mary Bech
APPLICANT: Carrer, Mary Bech
APPLICANT: Almquist, Ronald G.
APPLICANT: Ensinger, Carol Lee
TITLE OF INVENTION: CELL ADHESION INHIBITORS
FILE REFERENCE: 10274/024002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/983,391
CURRENT PILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR FILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-07-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTESEQ for Windows Version 4.0
SECTION NO.
                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America ZIP: 10020
                                                                                                                                                                                                  Sequence 1, Application US/08983391
Patent No. 6239108
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08498237
Patent No. 6248713
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Castro, Alfredo C
Zimmerman, Craig N
Cuervo, Julio H
                                                                                                                                                                                                                                                                                                                             Zimmerman, Craig N.
Cuervo, Julio Herman
  100.08;
                                                                                                                                                                                                                                                                                                                                                                      Lee, Wen-Cherng
Hammond, Charles E
                                                                                                                                                                                                                                                                                       Adams, Steven P.
Castro, Alfredo C.
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Adams, Steven P
  Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                  Lin, Ko-Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
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US-08-498-237-1
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APPLICANT:
                                                                                                                                                                                    JS-08-983-391-1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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| Sequence 3, Application US/09025622
| Patent No. 61943708|
| Patent No. 61943708|
| APPLICANT: Clark, Richard A |
| APPLICANT: Clark, Richard A |
| APPLICANT: Clark, Richard A |
| TITLE OF INVENTION: MATRIX FOR WOUND HEALING |
| VINDER OF SEQUENCES: 12 |
| CORRESPONDENCE ADDRESS: ADDRESSEE: Jackle Fleischmann & Mugel, LLP |
| STREET: 39 State Street |
| CITY: Rochester |
| STATE: New York |
| STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 4; Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/025,622
                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 3; I 100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE DOCKET NUMBER: 87653.97R270
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEPHONE: 716-262-4133
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
ZIP: 60601
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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                                                                                                                                                                                                                                                                                                                                  not relevant
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Best Local Similarity 100.vv
                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-130-225-56
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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APPLICANT: Wickham, Thomas J.
APPLICANT: Wickham, Thomas J.
APPLICANT: Wickham, Thomas J.
APPLICANT: Kovesdi, Imre
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
CORRESPONDENCE ADDRESS:
ADDRESSE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: 11linois
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUTY: USA
COMPUTER READABLE FORM:
MEDIUTY: USA
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
RAPOR APPLICATION NUMBER: US 9-130225
FILING DATE: 21-AUG-1998
RATORNEY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
REFERENCE/DOCKET NUMBER: 203128
INFORMATION FOR SEQ ID NO: 56:
COMPUTER READABLE CHARACTERISTICS:
COMPUTER TOWATERISTICS:
COMPUTER READABLE FORM:
APPLICATION NUMBER: 203128
INFORMATION FOR SEQ ID NO: 56:
COMPUTER TOWATERISTICS:
COMPUTER TOWATERISTICS:
COMPUTER TOWATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 4; I 100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56, Application US/09455061
Patent No. 6329190
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not relevant
                                             TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                      8 amino acids
                                                                                                                                                                                                                                      : peptide
NO
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MOLECULE TYPE: peptide
US-09-455-061-56
                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EILDV 5
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                                                                                                                                                                                                                 TOPOLOGY:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
CONFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURBENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498,237
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 1970
FILEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPAX: (212) 596-9000
TELEPAX: (212) 596-9000
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ZIP: 10020
ZIP: 10020
COUNTRY: United States of America
ZIP: 10020
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/376,372
FILING DATE:
CLASSIFICATION: 424
ATTONEY/AGENT INFORMATION:
NAME: Haley Jr. James F
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 21,794
REGISTRATION NUMBER: 21,794
REERERNCE/DOCKET NUMBER: B180
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Zimmerman, Craig N
APPLICANT: Zimmerman, Craig N
APPLICANT: Hammond, Charles E
APPLICANT: Liao, Yu.Sheng
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08376372
Patent No. 6306840
GENERAL INFORMATION:
APPLICANT: Adams, Steven P
APPLICANT: Lin, Ko-Chung
APPLICANT: Lie, Wen-Cherng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin, Ko-Chung
Lee, Wen-Cherng
Castro, Alfredo C
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Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION ATHEMA NEUROSCIENCES, INC.
TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHEMA NEUROSCIENCES, INC.
STREET: 800 Cateway Blvd.
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08516

FILING DATE: 10-JUL-1995

CLASSIFICATION NUMBER: BCT/US95/08516

FILING APPLICATION DATA:

APPLICATION NUMBER: US 08/273,055

FILING DATE: 11-JUL-1994

ATTORING APPLICATION NUMBER: US 08/273,055

FILING DATE: 11-JUL-1994

ATTORING APPLICATION NUMBER: 37,047

REGISTRATION NUMBER: 37,047

REGISTRATION NUMBER: 37,047

REGISTRATION NUMBER: 002010-008

TELEPHONE: (415) 87,0900
                                                                                                                                                                                                 OTHER INFORMATION: Synthetically generated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 5; I
ilarity 100.0%; Pred. No. 1.9e+05;
Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR FILING DATE: 1995-01-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAID.
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~WOTTER: IBM PC compatible
~~TOTTER: ~~CTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application PC/TUS9508516 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 877-3620 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 7
                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA
USA
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US-08-271-830-101
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MEDIUM TYPER FLOPAGE

MEDIUM TYPER: FLOPAGE

MEDIUM TYPER: FLOPAGE

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/039,780A

FILING DATE: 16-Mar-1998

CLASSIFICATION: «UNKNOWN»

ATTORNEY ARGISTRATION:

NAME: SULLIVAN, SALLY A.

REGISTRATION NUMBER: 32,064

REGISTRATION NUMBER: 32,064

REFERENCE/DOCKET NUMBER: 32-95C
                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
HAWLEY-NELSON, PAMELA
APPLICANT: HAWLEY-NELSON, PAMELA
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL OBLILAT
TITLE OF INVENTION PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 4; Length 8; 100.0%; Pred. No. 1.9e+05; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Caetro, Alfredo C.
APPLICANT: Zimmerman, Craig N.
APPLICANT: Hammend, Charles E.
APPLICANT: Hammond, Charles E.
APPLICANT: Liao, Yu-Sheng
APPLICANT: Cuervo, Julio Hernan
APPLICANT: Singh, Juswinder
TITLE OF INVENTION: CELL ADHESION INHIBITORS
FILE REFERENCE: 10274-023002
CURRENT APPLICATION NUMBER: US/08/875,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-039-780A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08875321
Patent No. 6376538
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Adams, Steven P.
APPLICANT: Lin, Ko-Chung
APPLICANT: Lee, Wen-Cherng
APPLICANT: Castro, Alfredo C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                 CITY: BOULDER
    RESULT 32
US-09-039-780A-48
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US-08-875-321-1
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Query Match
Best Local Similarity 100..
Best Local Si Conservative
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ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 BILDV 5
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US-08-338-282-6
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                                                                 APPLICANT: Kogan, Timothy P.
APPLICANT: Kogan, Timothy P.
APPLICANT: Ren, Kaijun
APPLICANT: Ren, Kaijun
APPLICANT: Vanderslice, Peter
APPLICANT: Beck, Pamela J.
TITLE OF INVENTION: A PROCESS OF INHIBITING THE BINDING OF THE
TITLE OF INVENTION: LINEAR PEPTIDES THEREFOR
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
STREET: 180 No. 5510332th Stetson, Suite 4700
CTTY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-435-286-3
; Sequence 3, Application US/08435286
; Patent No. 5688913th
; Patent No. 5688913th Stetson, Suite 4700
; Patent No. 5688913th Stetson, Suite 4700
; APPLICANT: Blices, Mariano J.
; APPLICANT: Blices, Mariano J.
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USING THE SAME; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/271,830

FLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5510332thrup, Thomas E.

REGISTRATION NUMBER: 33,268

TELECOMMUNICATION INFORMATION:

TELEFRONE: (312)616-5460

TELEFRAX: (312)616-5460

TELEFRAX: (312)616-5460

TELEFRAX: (312)616-5460

TELEFRAX: (312)616-5460

TELEFRAX: (312)616-5460

TELEFRAX: (312)616-5460

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LOCATION: 10
OUTER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa=Thr-NH2."
Application US/08271830
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MOLECULE TYPE: peptide
                              Patent No. 5510332
GENERAL INFORMATION:
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STATE: II
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
Sequence 101,
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Sequence 6, Application US/08338282
Patent No. 5730978
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
INUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
CITY: Seattle
CITY: Seattle
STATE: Washington
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REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEPRAX: 1-206-224-0779
TELERX: 4938023
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: Plan PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,286
FILING DATE:
CLASSIFICATION: 514
PRICA ASSIFICATION: DATA:
APPLICATION NUMBER: US/08/164,101
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
TELEPRATION NUMBER: 29,381
TELEPRATION FOR SEQ ID NO: 3:
SEQUENCE CRAAACTERISTICS:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CRAAACTERISTICS:
MANDEL DATA ACTORNEY/AGENTICS:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CRAAACTERISTICS:
MANDEL DATA ACTORNEY/AGENTICS
INFORMATION FOR SEQ ID NO: 3:
MANDEL DATA ACTORNEY/AGENTICS:
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SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
FILING DATE: CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Petent No. 5811391
GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Tempczyk, Anna
APPLICANT: Elices, Mariano J.
APPLICANT: Zhong, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Cyclic CS-1 Control Methods of Using Same NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    100.0%; Score 23; DB 1; Length 10; 100.0%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:

ADDRESSEER: campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
STATE: California
COUNTRY: United States
CONPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,077C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CY 1647
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 91,815
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REFERENCE/DOCKET NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 91,815
REGISTRATION SEQUED NO: 6:
                                                                                                                                                                                                                                               0; Mismatches
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US-08-519-109B-6
; Sequence 6, Application US/08519109B
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                                                                                                       MOLECULE TYPE: peptide
DESCRIPTION: GPEIL DVPST
US-08-338-282-6
                                           10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
HOLECULE TYPE: peptide
US-08-483-077C-6
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                                                                                         linear
                                                                  amino acid
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                                         LENGTH:
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Patent No. 6103870

GENERAL INFORMATION:
APPLICANT: Blices, Mariano J.
APPLICANT: Elices, Mariano J.
TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USING THE SAME COMMESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd. STREET: 180 No. 6103870th Stetson, Suite 4700

STATE: IL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                             APPLICANT: Elices, Mariano J.
APPLICANT: Zheng, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSES: Campbell & Plores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 2; Length 10;
100.0%; Pred. No. 9.7;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARES PATENTIN RAJESSES #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,109B
FILING DATE: 25-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-CY 1795
TELECOMMUNICATION INFORMATION:
                                                                                                                             LUNKESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Arrhenius, Thomas S.
Tempczyk, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (619) 535-9001
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Sequence 3, Application PC/TUS9510811
GENERAL INFORMATION:
APPLICANT: Cytel Corporation
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods For Using The Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 23; DB 5; Length 10; Best Local Similarity 100.0%; Pred. No. 9.7; Matches 5; Conservative 0; Mismatches 0; Indels
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COMPUTER: United States
21P: 9212
21P: 9212
21P: 9212
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARD: Patent In Release #1.0, Version #1.25
SOFTWARD: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10811
FILING DATE: 25-AUG-1995
CLASSIFICATION:
NAME: HOOK ATTON:
NAME: HOOK Gregory R.
REGISTRATION NUMBER: 38,701
REFERENCE/DOCKET NUMBER: 98-701
TELECHMONE: (619) 535-9901
TELEPAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIC
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 15
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13943
FILING DATE: 5-DCC-1994
SIGNEMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application PC/TUS9413943
GENERAL INFORMATION:
APPLICANT:
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MOLECULE TYPE: peptide
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STATE: California
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                                                         EILDV 5
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
FILING DATE:
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/923,026
                                                                                                                                                                                                                                                                                                                                                            ALICANAL FORMAT IN CONTROL OF A REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEPAX: (312)616-5400
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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FELECOMMUNICATION INFORMATION
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TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 10-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 5; Conservative
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STRANDEDNESS: Single
TOPOLOGY: Linear
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PCT-US95-08516-2
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US-08-190-130-3
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                                                                                        100.0%; Score 23; DB 5; Length 10; 100.0%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 3; Length 11; 100.0%; Pred. No. 11;
                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08467580B
| Patent No. 6001809
| GENERAL INFORMATION:
| APPLICANT: Thorsett. Eugene D
| APPLICANT: Pleiss, Michael A
| TILLE OF INVENTION: Inhibitors of Leukocyte Adhesion
| FILE REFERENCE: 123-US-CIP1
| CURRENT APPLICATION UNMBER: US/08/467,580B
| GARLIER APPLICATION NUMBER: 08/273,055
| EARLIER FILING DATE: 1994-07-11
| WIWHER OF SEQ ID NOS: 163
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9508516
GENERAL INFORMATION:
APPLICANT: ATHENA NEUROSCIENCES, INC.
TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
ADDRESSES: ATHENA NEUROSCIENCES, INC.
STREET: 800 Gateway Blvd.
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/08516
                                                                                                                               0; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORGANISM: Artificial Sequence
                                                                                                          Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
             TOPOLOGY: linear
MOLECULE TYPE: peptide
amino acid
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LOCATION: (1)
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4 EILDV 8
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PCT-US95-08516-2
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                                                    PCT-US95-10811-3
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US-08-467-580-2
                                                                                        Query Match
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Patent No. 5628979

GENERAL INFORMATION: Alan William John

TITLE OF INVENTION: No. 5628979el Reagent For Tumour

TITLE OF INVENTION: Inaging and Therapy

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fay, Sharpe, Beall, Fagan,

ADDRESSEE: Minnich & McKee

STREET: Suite 700

STREET: Suite 700
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,055
FILING DATE: 11-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERRNCE/DOCKET NUMBER: 002010-008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 877-0900
TELEFAX: (415) 877-0900
TELEFAX: (415) 877-0500
TELEFAX: (415) 877-0500
TELEFAX: (415) 877-0500
TELEFAX: (415) 877-0500
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STATE: Ohio
COUNTRY: Cleveland
COUNTRY: U.S.A.
ZIP: H414-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: Diskette, 3.50 inch,
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MEDIUM TYPE: DISKette, 3.50 inch,
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GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Brices, Mariano J.
APPLICANT: Elices, Mariano J.
APPLICANT: Elices, Mariano J.
APPLICANT: Cheng, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STREET: California
COUNTRY: United States
IP: 92122
COMPURER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEADATING SYSTEM: PC-DOS/MS-DOS
CORPUTER: DEADATING SYSTEM: PC-DOS/MS-DOS
CORPUTER: DEADATING SYSTEM: PC-DOS/MS-DOS
CORPUTER: DEADATING SYSTEM: PC-DOS/MS-DOS
CORPUTER: DEADATING SYSTEM: PC-DOS/MS-DOS
CORPUTER: DEADATING SYSTEM: PC-DOS/MS-DOS
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CORPUTER: DEADATING STATEM: PC-DOS/MS-DOS
CORPUTER: DEADATING STATEM: PC-DOS/MS-DOS
CORPUTER: DEADATI
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                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION 1424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTORNEY/AGRNT INFORMATION:
NAME: Sundamo,John,8.
REFERENCE/DOCKET NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 1-206-682-8100; 1-206-224-0727 (direct)
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IEM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOPTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
DESCRIPTION: 812; Fig. 9B;LHGPE ILDVP ST
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FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08483077C Patent No. 5811391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 4938023
INFORMATION FOR SEQ ID NO:
                            Seattle
Washington
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                                                                                       COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Wayner, E.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
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                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08435286
Patent No. 568913
GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Gaeta, Federico C.A.
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Desesler, Goldsmith, Shore & Milnamow, Ltd.
STREET: 180 No. 5688913th Stetson, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOSITIONS AND
                         DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 1; Length 12; 100.0%; Pred. No. 12;
                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER PORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
APPLICATION NUMBER: US/08/164,101
                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                         100.0%; Score 23; 100.0%; Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 48
US-08-338-282-5
Sequence 5, Application US/08338282
; Patent No. 5730978
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ATTORNEY/AGENT INFORMATION:
                                                        Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60601
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5 EILDV 9
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US-08-435-286-2
                            Query Match
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0; Gaps

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Sequence 2, Application US/08923026

Patent No. 6103870

GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Blices, Mariano J.
APPLICANT: Gaeta, Federico C.A.
TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, STREET: 180 No. 6103870th Stetson, Suite 4700 CITY: Clicago STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29, 381
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60601
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US-08-923-026-2
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US-08-837-154-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Tempozyk, Anna
APPLICANT: Tempozyk, Anna
APPLICANT: Tempozyk, Anna
APPLICANT: Tempozyk, Anna
APPLICANT: Zheng, Zhong-Li
APPLICANT: Zheng, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPEDUBRING ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STREET: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,109B
FILING DATE: 25-AUG-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CY 1647
TELECOMMUTICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9049
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-077C-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CY 1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 12 amino acids
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Best Local Similarity 100.
Matches 5; Conservative
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MOLECULE TYPE: peptide
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100.0%; Score 23; DB 3; Length 12; 100.0%; Pred. No. 12;
                                          0; Indels
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Patent No. 6117840
GENERAL INFORMATION:
APPLICANT: Attrentus, Thomas S.
APPLICANT: Elices Mariano J.
APPLICANT: Gaeta. Federico C.A.
ATILE OF INVENTION: AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
STREESSES: Welsh & Katz, Ltd.
STREET: 135 South La Salle Street, Suite 1625
                                          0; Mismatches
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STATE: IL
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Gaps
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TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods For Using The Same
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                    CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 5; Length 12;
Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                       TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIO
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 15
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13943
FILLING DATE: 5-DEC-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 25-AUG-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
12;
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Pred. No.
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NAME: HOOK, Gregory R.
REGISTATION NUMBER: 38,701
REFERENCE/DOCKET NUMBER: FP-CY 1778
TELECOMMUNICATION INFORMATION:
Sequence 2, Application PC/TUS9413943
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9510811 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4370 La Jolla VI
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
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LENGTH: 12 amino acid
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MOLECULE TYPE: peptide
PCT-US94-13943-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // MOLECULE TYPE: peptide
PCT-US95-10811-2
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TOPOLOGY: linear
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Best Local Similarity
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APPLICANT:
TITLE OF INVENTION: INTEGRIAN...

TITLE OF INVENTION: ENHANCED TRANSFECTION...

TITLE OF INVENTION: ENHANCED TRANSFECTION...

COMPUTER READABLE FORM:

COMPUTER: ISP PC compatible

COMPUTER: ISP PC compatible

COMPUTER: TEM PC compatible

COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30 (BPO)
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,154
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PATENTIN NO. CURRENT ARE: PATENTIN DATA:
APPLICATION NUMBER: US/09/424,656
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9711115.7
FILING DATE: 29-MAY-1997
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARATERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    APPLICAL.
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEFAX: (312)781-9470
TELEFAX: (312)781-9548
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 6458026
GENERAL INFORMATION:
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Best Local Similarity
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RESULT 53

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RESULT 54

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                                                                                                                                        RESULT 58
US-08-701-124-59
is Sequence 59, Application US/08701124
is Patent No. 5846782
is General INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIPS
INTRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Ploor CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                        Query Match 100.0%; Score 23; DB 2; Length 21; Best Local Similarity 100.0%; Pred. No. 21; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 23; DB 2; Length 21; Best Local Similarity 100.0%; Pred. No. 21; Matches 5; Conservative 0; Mismatches 0; Indels
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Sequence 57, Application US/09130225
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Wickham, Thomas J.
APPLICANT: Kovesdi, Imre
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acide
; MOLECULE TYPE: peptide US-08-701-124-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // MOLECULE TYPE: peptide
US-08-701-124-59
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, OTHER INFORMATION: Description of Artificial Sequence: Linker
US-09-367-9538-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 4; Length 18; 100.0%; Pred. No. 18; tive 0; Mismatches 0; Indels
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Patent No. 5846782

GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: ROELVINK:
APPLICANT: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
  0; Indels
                                                                                                                                                                             Sequence 25, Application US/09367953B
Patent No. 6287572
GENERAL INFORMATION:
APPLICANT: Kingsman, Alan J
APPLICANT: Kingsman, Alan J
TITLE OF INVENTION: Anti-HIV peptides and proteins
FILE REPERENCE: 550-154
CURRENT APPLICATION UNMBER: US/09/367,953B
CURRENT FILING DATE: 1999-08-24
PRIOR FILING DATE: 1999-08-24
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  0; Mismatches
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FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
5; Conservative
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STRANDEDNESS: sir
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                                                                                                                                          RESULT 56
US-09-367-953B-25
                                         1 EILDV 5
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US-08-701-124-57
Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 3; Length 21; 100.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 59, Application US/09130225
; Sequence 59, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
    APPLICANT: Wickham, Thomas J.
    APPLICANT: Wockedi, Imre
    TILLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
    TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE LEYGIG, Voit & Mayer, Ltd.
    STREET: Two Prudential Plaza - 49th Floor
    CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMET Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LEMGTH: 21 maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 amino acids
                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-09-130-225-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
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Matches 5; Conserva
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US-09-130-225-59
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Gaps
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Pred. No. 21;
                                                                                APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Rovelvink, Petrus W.
APPLICANT: Rovelvink, Targering Abenovirus WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mickham, Thomas J.
APPLICANT: Relvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roverdi, Imres W.
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS CORRESPONDENCE ADDRESS: ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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CMEDURE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOUTHWER: PATENTIN Release #1.0, Version #1.30

SUGTAMER: PATENTIN Release #1.0, Version #1.30

SUGTAMER: PATENTIN Release #1.0, Version #1.30

SUGTAMENT APPLICATION DATA:

APPLICATION NUMBER: US/09/455,061

FILING DATE: 06-AUG-199

FILING DATE: 06-AUG-199

FILING DATE: 10-AUG-199

FILING DATE: 21-AUG-199

FURMEY/AGRAT INFORMATION:

NAME: Hefner, M. Daniel

REFERENCE/DOCKET NUMBER: 203128

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTER.ESTICS:
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Sequence 57, Application US/09455061
Patent No. 6329190
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 62
US-003-455-061-59
Sequence 59, Application US/09455061
Patent No. 6329190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-455-061-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Ouery Match
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                     100.0%; Score 23; DB 1; Length 24; 100.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08291349A
Patent No. 5545620
GENERAL INFORMATION:
APPLICANT: Wall, Sharon M.
APPLICANT: MCCarthy, James B.
APPLICANT: Furcht, Leo T.
ITLE OF INVENTION: Inhibitors of Retroviral Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: The PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 16 AUG 1994
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/006,121
FILING DATE: 19 JAN 1993
CLASSIFICATION 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 26,613-B
TELEPONMULICATION INFORMATION:
TELEPONMULICATION: 112-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "FN6 (1961-1985)
fibronectin fragment : CS-1"
                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff
STREET: 10 S. Wacker Drive
CITY: Chicago
STATE: 1111nois
TOPOLOGY: linear
US-08-453-378-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERASTICS:
LENGTH: 25 amino acids
                                                                                                                                                                           Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: Bingle
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
LOCATION: 1..25
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                           17 EILDV 21
                                                                                                                                                                                                                                                  1 EILDV 5
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                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                  RESULT 64
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Sequence 2, Application US/08453378

Patent No. 561648

GENERAL INFORMATION:

APPLICANT: Salmi, Marko

APPLICANT: Salmi, Marko

APPLICANT: Jalkanen, Sirpa

TITLE OF INVENTION: Compositions And Diagnostic Methods

TITLE OF INVENTION: Using Monoclonal Antibodies Against CD44v6

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSES: Sterne, Kessler, Goldstein & Fox

STRET: 1100 New York Avenue Suite 600

CITY: Washington

STRET: 1100 New York Avenue Suite 600

CITY: Washington

STRET: 1100 New York Avenue Suite 600

COUNTRY: U.S.A.

IP: COUNTRY: U.S.A.

ZIP: Z0005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,378

FILING DATE:

CLASSIFICATION NUMBER: US/08/453,378

FILING DATE:

CLASSIFICATION NUMBER: US/08/453,378

FILING DATE:

FILING DATE:

REFERENCE/OCKET NUMBER: 1102.0070000

TELECOMMUTICATION INDRER: 1102.0070000

TELECOMMUTICATION INDRER: 1102.0070000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/455,061
FILING DATE: 06-DEC-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9-130225
FILING DATE: 12-10-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFRENCE/DOCKET NUMBER: 20312
INPORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: alinear
MOLECTLE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EILDV 5
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FITLE OF INVENTION: Imaging and Therapy
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: Amino Acid
STRANDEDNESS: Siz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 EILDV 22
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                                                                                                                                                                                          Sequence 4, Application US/07990296

Patent No. 559179

GENERAL INFORMATION:

APPLICANT: Furcht, Leo T.

APPLICANT: Allen, Janice B.

APPLICANT: Allen, Janice B.

APPLICANT: Allen, Janice B.

APPLICANT: Mall, Sharon M.

APPLICANT: Wall, Sharon M.

TITLE OF INVENTION: Method for Treating Acute and

TITLE OF INVENTION: With Fibronectin Activity

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: Merchant & Gould

STREET: 3100 No. 5591719west Center

CITY: Minneapolis

CORRESPONDENCES:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 25, 100.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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No. 5628979el Reagent For Tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/990,296
FILING DATE: 19921210
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchyk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600.252-US-01
TELEPHONE: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acid residues
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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FRAGMENT TYPE: Internal Fragment
ORIGINAL SOURCE: Synthetically Derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 66
US-08-190-130-1
Sequence 1, Application US/08190130
Patent No. 5628979
GENERAL INFORMATION:
APPLICANT: STUTTLE, Alan William (TITLE OF INVENTION: No. 5628979e1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
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18 EILDV 22
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COCATION:
COCATION:
US-07-990-296-4
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NAME/KEY:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                               US-07-990-296-4
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100.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches n. Train
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| Sequence 4, Application US/08190130|
| Patent No. 5628979
| GENERAL INFORMATION:
| TITLE OF INVENTION: Imaging and Therapy TITLE OF INVENTION: Imaging and Therapy TOTALE OF INVENTION: Imaging and Therapy MADRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Ray, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee STREET: 1100 Superior Avenue CITY: Cleveland STREET: Suite 700
| CITY: Cleveland STREET: Suite 700
| CITY: Cleveland STREET: Suite 700
| COUNTRY: U.S.A. ZIP: 44114-2518
| COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM TYPE: TOR KE STORD: COMPUTER: IBM PS/2, Model 35 SX OPERATING SYSTEM: DOS 5.0
| SOFTWAREN: WORD PERFECT 5.1
| CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/190,130
AUTORES OF SEQUENCES: GORRESPONDENCES: GORRESPONDENCES: GORRESPONDENCES: GORRESPONDENCES: GORRESPONDENCES: Mannich & McKee STREET: 1100 Superior Avenue STREET: 1100 Superior Avenue STREET: 1100 Superior Avenue STREET: 0010 COUNTRY: Cleveland STATE: Ohio COMPTRY: U.S.A.

ZIP: 44114-2518
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM TYPE: Diskette, 3.50 inch, MEDIUM SYSTEM DOS 5.0 SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: Diskette, 3.1994
CLASSIFICATION NUMBER: US/08/190,130
FILLING DATE: June 13, 1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24,175
RESFERENCE/DOCKET NUMBER: 24,175
RESFERENCE/DOCKET NUMBER: XOU 2 042
TELEFORMULICATION INFORMATION:
TELEFORM. (216) 861-5582
TELEFORM. (216) 861-5582
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GENERAL INFORMATION:
APPLICANT: Wayner, B.A.
TITLE OF INVENTION:
INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide
CS-1 domain; Fig. 9A;DELPQ LVTLP HPNLH GPEIL DVPST
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                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sundsmo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECOMMULICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEPRAX: 1-206-224-0779
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-658-130-20
; Sequence 20, Application US/08658130
Patent No. 5736392
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hawley-Nelson, Pamela
APPLICANT: Lan, Jianging
APPLICANT: Shih, Poden
APPLICANT: Jessee, Joel A.
100.0%; Pre
                                                                                                                                                                                                                        Sequence 2, Application US/08338282
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
              Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
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DESCRIPTION:
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Sequence 1, Application US/08435286

Sequence 1, Application US/08435286

Patent No. 5688933

PAPELICANT: Arrhenius, Thomas S.

APPLICANT: Blices, Mariano J.

APPLICANT: Gaeta, Febrico C.A.

TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USING THE SAME

NUMBER OP SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 25; 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEB: Dressler, Goldsmith, Shore & Milnamow, Ltd.
STREET: 180 No. 5688913th Stetson, Suite 4700
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                            ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: 20,002 042
TELECOMMUNICATION INFORMATION:
TELEFAX: (216) 861-582
TELEFAX: (216) 241-1666
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE GHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23;
100.0%; Pred. No. 3
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
                 June 13, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100...
5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                           TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                 FILING DATE: Ju
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COUNTRY: USA
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| Patent No. 5824547
| GENERAL INFORMATION:
| APPLICANT: HASHINO, Kimikazu
| APPLICANT: MATGUSHITA, Hideyuki
| APPLICANT: KATO, Ikunoshin
| TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
| NUMBER OF SEQUENCES: 21
| CORRESSONDENCE ADDRESS:
| ADDRESSEE: Browdy and Neimark
| STREET: 419 Seventh Street N.W. Ste. 300
| CITY: Washington
| STATE: D.C.
| STATE: D.C.
| CONNEY OSA
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
FLING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAMME: BLOWDY: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAMME: BLOWDY: 25,618
REGISTRATION NUMBER: 45,618
REGISTRATION NUMBER: 45,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTER STILES:
TENERAL (202) 737-3528
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTER STILES:
                                                                               APPLICATION NUMBER: US/08/483,077C
GLASSIFICATION NUMBER: US/08/483,077C
GLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION INFORMATION:
TELECHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: siz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 EILDV 22
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US-08-836-854-2
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| Patent No. 5811391
| GENERAL INFORMATION:
| APPLICANT: Tempczyk, Anna |
| APPLICANT: Tempczyk, Anna |
| APPLICANT: Thempczyk, Anna |
| APPLICANT: Thempczyk, Anna |
| APPLICANT: Thempczyk, Anna |
| TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics, |
| TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics, |
| TITLE OF INVENTION: Compositions and Methods of Using Same |
| VIMBER OF SEQUENCES: 33 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Campbell & Flores LLP |
| STREET: 4370 La Jolla Village Drive, Suite 700 |
| CITY: San Diego |
| CONTYR: United States |
| COMPUTER READABLE FORM: |
| MEDIUM TYPE: EN PORPY disk |
| COMPUTER: IBM PC Compatible |
| COMPUTER: DEACONDENCE |
| COMPUTER: PREFERENCE |
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APPLICANT: Shifferli, Kevin P.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
TITLEO OF INVENTION: Transfections
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,130

FILING DATE: 04-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/477,354

FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATULHERS, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET WUMBER: 32-95A
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LEMGTH: 25 amino acids
TVENGTH 25 amino acids
TVENGTH 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 5; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                         APPLICANT: Furcht, Leo T.
APPLICANT: McCarthy, James B.
APPLICANT: Wahl, Sharon M.
APPLICANT: Wahl, Sharon M.
APPLICANT: Allen, Janice B.
APPLICANT: Billups, Kevin L.
APPLICANT: Brocett, Jeffrey E.
TITLE OF INVENTION: Method for Treating Inflammatory
TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Comits
STREET Merchant & Comits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5840691west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 2; Length 25; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels
                                                               Query Match 100.0%; Score 23; DB 2; Length 25; Best Local Similarity 100.0%; Pred. No. 26; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: MINICAPOLIS

COUNTRY: USA

ZIP: 55402

COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,133A

FLING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,903

FILING DATE: 21-OCT-1993

PRIOR APPLICATION NUMBER: US 08/139,903

FILING DATE: 10-OCT-1993

PRIOR APPLICATION NUMBER: US 07/990,296

FILING DATE: 10-DEC-1993

ATPLICATION NUMBER: US 07/990,296

FILING DATE: 10-DEC-1993
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                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08480133A Patent No. 5840691 GENERAL INFORMATION: APPLICANT: MCCARTHY, James B. APPLICANT: MCCARTHY, James B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFRENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEPAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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MOLECULE TYPE: peptide

// MOLECULE TYPE: peptide
US-08-836-854-2
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18 EILDV 22
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Best Local S
Matches 5
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GREEAL INFORMATION:

APPLICANT: Archenius, Thomas S.
APPLICANT: Archenius, Thomas S.
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APPLICANT: Archenius, Thomas S.
APPLICANT: Archenius, Thomas S.
APPLICANT: Archenius, Thomas S.
APPLICANT: Block, Mariano J.
APPLICANT: Block, Mariano J.
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APPLICANT: Block, Mariano J.
APPLICANT: Block, Mariano J.
APPLICANT: Block, Mariano J.
APPLICANT: Block, Mariano J.
ADDRESSES: Campbell & Flores Lip
STERET: 4370 La 2031a Village Drive, Sulte 700
STATE: California
CONFRY: United States
APPLICANTON MARS: Thomas C.
APPLICANTON MARS: Thomas C.
SOUTHARE: Partent Release #1.0, Version #1.25
APPLICATION MARS: Thomas C.
SOUTHARE: All APPLICATION MARS: All APPLICATION MARS: A manh acids
APPLICATION MARS: A manh acids
TELERONE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 87653.97R263
TELEPHONE: 716-262-3640
TELEPHONE: 716-262-3640
ITELEPHONE: 716-262-3640
ITELEPHONE: 716-262-3640
INFORMATION OF SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 25 anino acid STRANDEDNESS:
MOLECULE TYPE: amino acid STRANDEDNESS:
MOLECULE TYPE: peptide
US-09-025-706-4
QUETY MATCH
QUETY MATCH
QUETY MATCH
MATCHES 5; CONSELVATIVE 0; MAISMATCHES 0; Indels 0; Gaps 0;
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Search completed: February 8, 2003, 10:25:20 Job time : 16 secs

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